Planning National Programmes for Conservation of Forest Genetic Resources

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Publication date:
1997

Document version
Publisher's PDF, also known as Version of record

ISSN 0902-3224

Technical Note No. 48 - December 1997

Planning national programmes for conservation of forest genetic resources

by

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Reader's guide

This Technical Note is intended for managers, administrators, planners and researchers involved in planning and implementation of national programmes for conservation of forest genetic resources.

The executive summary, page v-ix, provides an overview of the various steps in planning and implementing forest genetic resource conservation. Chapter 1 gives a brief description of the need and justification of such programmes and provides an introduction to aspects of terminology, methodology and organisation.

Chapters 2-8 go through the following sequence of activities:

- Selection of priority species
- Assessment of their genetic variation
- Assessment of their conservation status
- Identification of populations to be conserved
- Identification of conservation measures
- Planning and organisation of specific conservation activities
- Preparation of management guidelines

The chapters are fairly short and straightforward with chapter 3 and 6 as exceptions. Chapter 3 deals in some detail with the concept of genecological zonation, which is central to the identification of conservation requirements. Chapter 6 gives a broad description of different conservation options and their feasibility for conservation of genetic resources.

In the note, boxes are used for explanation of terminology and subjects considered of specific importance. Practical examples covering different species and different countries are provided. Two of the examples are used throughout the note to illustrate the whole process of planning. One deals with conservation of genetic resources of teak (Tectona grandis) in Thailand, and the other covers a larger number of selected species in the Sudan. The examples are written with small print to distinguish them from the general text.

A large number of references are quoted, including many with examples that may be of inspiration for specific cases of national genetic resource conservation. Some references are of a more general nature and may be useful to have at hand when preparing national gene resource conservation plans, e.g. FAO (1989), Guarino et al. (1995), Frankel et al. (1995) and Maxted et al. (1997).

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Abbreviations

CAB	Commonwealth Agricultural Bureau
CIDA	Canadian International Development Agency
CRF	Centre de Recherches Forestières, Cameroon
Danida	Danish International Development Assistance
DFSC	Danida Forest Seed Centre
FAO	Food and Agriculture Organisation of the United Nations
FNC	Forests National Corporation, Sudan
IBPGR	International Board for Plant Genetic Resources (now IPGRI)
IPGRI	International Plant Genetic Resources Institute (earlier IBPGR)
ISTA	International Seed Testing Association
IUCN	World Conservation Union (International Union for the Conservation of Nature and Natural Resources)
NGO	Non Governmental Organisation
NRC	National Research Council, Washington D. C.
RFD	Royal Forest Department, Thailand
TSP	Tree Seed Project, Sudan
UNEP	United Nations Environment Programme
WWF	World-wide Fund for Nature (earlier World Wildlife Foundation)

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Executive summary

1. Introduction

The objectives of conserving forest genetic resources are to secure the ability of forest tree species to adapt to environmental changes and to maintain the basis for improving production and other benefits of growing trees.

Forests are disappearing quickly in many parts of the world. Among the consequences are loss of genetic resources of many forest tree species which may threaten their survival or their possible use in the future. Many countries would therefore, both in the short and the long term, benefit from a systematic approach to planning and implementation of national forest gene conservation programmes.

The present note provides a practical framework for such planning. The sequence of activities described is:

- Selection of priority species
- Assessment of their genetic variation
- Assessment of their conservation status
- Identification of populations to be conserved
- Identification of appropriate conservation measures
- Organisation and planning of specific conservation activities
- Preparation of management guidelines for the objects of conservation

2. Selection of priority species

The identification of important genetic resources is a cost/benefit consideration. The main criteria for including species in genetic resource conservation programmes are their present and their possible future use. There are at least three different ways of assessing priority: (i) Survey of planting areas and value production in planting programmes, (ii) Market survey of forest products consumption, and (iii) User preference measurements. Whenever possible, the three approaches should be combined to give a realistic and valid impression of species priorities. It is especially important to examine carefully the potential of highly valuable species, which may contribute only little to the economy simply because they are rare. Also, the value of locally used species, which are not traded at high prices on international markets, should not be underestimated. Such species may be of major importance for the subsistence of local populations in rural areas.

Efforts should also be taken to conserve endangered species, even if they are seen as having little or no utilisation value. However, conservation of such species will typically be integrated in more general nature conservation programmes.

3. Assessment of genetic variation

Reliable information on the distribution of genetic variation - within and between geographic regions - is important in order to establish an effective network of conservation populations. The genetic variation of a species can be assessed by different techniques. It is possible to study morphological and metric characters in field trials, biochemical and molecular markers in the laboratory, and to guess on possible genetic variation patterns from ecogeographic variation. Both field trials and laboratory studies are expensive and time consuming. For most species, conservation of their genetic resources will therefore initially have to rely on an assessment of the ecogeographic variation of their distribution area.

The tool used is referred to as genecological zonation. A genecological zone can be defined as an area with sufficiently uniform ecological conditions to assume similar phenotypic or genetic char-

acters within a species. Such zonation is based on a compromise between the variation in ecological factors and expectations of gene flow. The zones should not be too small, because pollen flow between neighbouring zones would then be likely to prevent that any genetic differences develop between populations from the different zones. On the other hand, the zones should not be too large, because then important genetic differences may exist between populations within each zone. A zonation system may be prepared as one common system for all species considered, groups of similar species, or even single species. Factors typically used for zonation are natural vegetation, topography, climate, and soil as well as barriers to pollen and seed dispersal.

4. Assessment of conservation status

Conservation status refers to the present state of the genetic resources and the risks of depletion in the future. Questions to examine are: Have populations been lost? How well protected are remaining populations? And have remaining populations been subject to genetic erosion?

The conservation status of species and their populations may be used as an indicator for setting priorities in itself. We prefer to assess present or potential value first, and then the conservation status as a basis for identifying required conservation measures.

Assessment of the conservation status of a species and its populations will have to be based on knowledge of (i) past and present geographical distribution, (ii) prevailing utilisation patterns in the form of harvesting, planting and breeding of the species (including introduction of intercrossing species/provenances) or indirectly through changing land use patterns, and (iii) its possible occurrence in protected areas.

5. Identification of populations to be conserved

By comparing the genecological zones and the conservation status of a species, it is in principle possible to identify the conservation requirements in terms of the geographical distribution and the number of areas to be sampled for conservation of genetic resources. All major gene pools should be conserved, but the number of conservation stands should on the other hand be limited to a manageable level. The number of zones where a species occurs will provide an indication of the number of populations to be conserved.

In practice the comparison of genecological distribution and conservation status will typically consist of several steps:

- Overlay the genecological zones with:
- The natural and present geographical distribution of the species
- The occurrence of the species in planting programmes and protected areas
- Location of provenances that are known to be valuable

II. Consider factors affecting the genetic variation, conservation status, and the conservation investment requirements:

- Type of distribution area
- Reproduction and distribution biology
- Differences between past and present distribution
- Size and geographical location of planting programmes, and origin of the planting material used
- Possible effect of selective exploitation in each zone
- Occurrence of populations in protected areas
- Security requirements
- Land tenure and associated options and costs

III. Decide on appropriate geographical distribution and number of areas per zone to be conserved or sampled for conservation of genetic resources.

Step I may be characterised as data collection and mapping, step II as interpretation, and step III as decision.

6. Identification of appropriate conservation measures

Selection of conservation method depends primarily on the objectives of conservation. The conservation options in the form of possible conservation methods may be limited by the biological nature of the material to be conserved, the socio-economic context of its habitats and the costs associated with the different methods. The preferred approach to conservation of genetic resources in forestry is to maintain evolutionary conservation populations in the form of living stands, preferably *in situ*, but also *ex situ*. In such populations, the genetic composition of target species is allowed to adapt to the prevailing environmental conditions and their change with time. Climatic changes at a given site may thus be responded to by corresponding adaptation of the local conservation populations to the new conditions through natural selection in favour of the fittest trees.

Static conservation maintains specific genetic compositions, e.g. in the form of seed lots or gametes in long term storage in gene banks or vegetatively propagated clones in clone collections. Well defined genetic material can thus be conserved with their present genetic composition as no changes - in principle - should take place in static conservation. To the extent that static conservation is required, it will often be taken care of by breeding programmes.

Conservation of genetic resources often requires simultaneous use of several methods. For economic reasons and when evaluating security, *ex situ* conservation or a combination of *in situ* and *ex situ* methods will usually be considered. *Ex situ* conservation of seed, pollen or tissue in gene banks will often be important complementary activities. However, the long period of time and the large areas required for regeneration, generally make *ex situ* storage less feasible for evolutionary conservation of woody perennials.

7. Organisation and planning of specific conservation activities

When a genetic resource conservation programme is being planned, it is important to consider (i) who is going to take care of the programme and who else is supposed to be involved, and (ii) what is going to happen in practice (implementation planning).

Organisation

Areas where genetic resources of common interest occur may be owned and used by different individuals, communities or public organisations. The organisation of conservation may therefore be complex.

The distribution of species and ecosystems do not respect national boundaries. Conservation of genetic resources in one country may often be to the benefit of other countries, where the species are presently grown or have future potential. The potential benefit of international co-operation between national programmes for conservation of genetic resources is thus quite obvious. Nevertheless it is from a practical point of view necessary initially to adopt a national approach, as a basis for international collaboration.

The development of national strategies for conservation and utilisation of forest genetic resources is an important step in defining the most appropriate organisational set-up and the allocation of responsibilities to relevant institutions, whether existing or new ones. An appropriate structure of such programmes may, however, vary a lot and it is thus not possible to suggest one model for implementation.

Implementation planning

It is important to know the different stakeholders of forest genetic resources, their possible organisation and economic capacity. Major points to consider in relation to the areas identified for conservation are tenure rights, and the herewith associated options and costs of administration and management. When specific populations have been identified for conservation, the next step is to decide which conservation measures to apply and who should implement them.

Concerning measures, the types of question to answer are: should a given population be demarcated and guarded? Should reproductive material be collected and put in store? Or should it be used for establishment of a new plantation? Or should we use some of these measures in combination? Do we have to consider pure conservation populations or can we combine conservation with some form of utilisation, e.g. seed supply?

Implementing conservation of genetic resources will in general need specialised structures with specific requirements both in terms of infrastructure and staff. Requirements depend on the types and amounts of genetic resources to be handled and on the allocation of tasks among collaborating partners. Different units and administrative bodies with vested interests may typically already exist and will usually have important roles to play.

8. Preparation of management guidelines for the objects of conservation

From a management point of view it is practical to distinguish between two major groups of conservation methods: conservation stands and gene banks.

Conservation stands

Conservation stands are of particular relevance for conservation of genetic resources of trees. The need for management and the specific management interventions required will vary with species and site-specific characteristics of each stand.

Crucial (more or less) manageable factors for conserving the genetic variation of a stand are: (i) size and family structure, (ii) regeneration, isolation and tending, (iii) utilisation, and (iv) site conditions.

The size of a conservation population will depend on species and site-specific conservation aspects. Mixed stands in which the objective is to conserve the genetic variation of one or more species will in general have to be larger than pure stands. As a rule of thumb, an *in situ* stand of a wind pollinated species should initially consist of at least 150 and preferably more than 500 interbreeding individuals of each of the species to be conserved. Final stand size should be 500-1500 individuals or more per species. Seed collection from one species in a stand for the purpose of establishing an *ex situ* stand should involve at least 150 trees if their relationship is unknown. Seed should be collected from at least 25 randomly chosen and supposedly unrelated individuals. If the individuals in the mother stand are supposedly unrelated, the rule of thumb is that it should consist of at least 50 trees. When establishing *ex situ* conservation stands, the aim should be a final stand size of 500-1500 individuals or more. The different numbers are based on population genetic considerations.

The conservation stands should be regenerated with as little genetic influence from outside as possible. In practice this requires isolation. Isolation belts of 300-500 m is generally recommended. When tending is required, it should favour stability and regeneration. For some populations the conservation effort will consist of a certain management system, which may include e.g. cutting of competitive species or for certain bushes, controlled animal grazing or fire. Thinning is generally considered the most important tending intervention, in particular where it stimulates regeneration. In pure stands where evolutionary conservation is the purpose, thinning should in principle support naturally selective forces and may therefore not be purely systematic. In mixed stands, thinning and regulation of species composition should be undertaken with much caution as it can be of more harm than use.

In some cases, the conservation effort can be combined with different forms of forest utilisation, if the use does not change the genetic constitution of the stands markedly. In some cases, conservation may be combined with ordinary forest management.

For *in situ* conservation and where existing stands are being considered as *ex situ* conservation stands, site conditions are of course given. The conservation status and the expected long term development will be taken into consideration in the process of selecting such stands for conserva-

tion. For *ex situ* stands to be established, areas that will ensure good protection as well as healthy long term development should be chosen. Environmental conditions should be as similar to the original as possible. Land tenure conditions will have to be taken into consideration as well.

Gene banks

Ex situ conservation of forest genetic resources in gene banks is an important complementary measure to the use of conservation stands. The term 'gene bank' may have a connotation of 'high tech'. It is however not necessarily the case. Fairly simple storage facilities can be used for *ex situ* conservation of many species and are often available. More specialised structures may be required in some cases and may only be available at international level. Documentation requirements and methodology are in principle the same. Managing the collections for conservation and use may include: collection, monitoring storage conditions, viability monitoring, regeneration and multiplication, characterisation and evaluation, and documentation and information.

1. Introduction

1.1 The need for conservation of genetic resources and conservation planning

Forests are disappearing quickly in many parts of the world (FAO 1993, 1995). Among the consequences are loss of genetic resources of many forest tree species which may threaten their survival or their possible use in the future. Most countries with major pressure on their forest land would therefore, both in the short and the long term, benefit from a systematic approach to planning and implementation of national forest gene conservation programmes. However, only few such programmes exist and practical experience in planning and implementation of genetic resource conservation is limited.

The present note provides a practical framework for national gene conservation planning. The approach proposed is based on genecological zonation coupled with an assessment of the socio-economic value of species, their conservation status (including geographical distribution and distribution history, present utilisation patterns and management practises), and reproductive biology. Major technical terms used in the note are defined in box 1.

1.2 Objectives of genetic resource conservation

Genetic diversity is one aspect of biological diversity. The objectives of the Convention on Biological Diversity agreed upon in Rio in 1992 refers to intrinsic as well as utilitarian values of biological diversity including their importance for evolution and for maintaining life-sustaining systems (Glowka et al. 1994).

In general, the objectives of conserving forest genetic resources are to secure the ability of forest tree species to adapt to environmental changes and to maintain the basis for improving production and other benefits of growing trees through future selection and breeding activities (cf. e.g. FAO 1989). Conservation activities will thus support future efforts of providing appropriate reproductive material for tree planting purposes. Only through such long term conservation programmes can it be secured that suitable reproductive material continuously can be made available in the future. Within the context of national tree seed programmes, emphasis will usually be on conserving seed sources of priority species in prevailing planting programmes that are appropriate for principal planting sites and desired end uses (Graudal and Moestrup 1997). However, the main criteria for including species in genetic resource conservation programmes are both their present and their possible future use.

The focus of gene resource conservation is thus on utilitarian values of evolution and human use. Despite this more narrow focus of gene resource conservation compared to conservation of biological diversity, conservation of genetic resources may in some cases imply conservation of ecosystem structure and function where priority species depend thereon (cf. section 6).

1.3 The concept of genetic resources and the dilemma of conservation

The definition of genetic resources (cf. box 1) implies emphasis on the usefulness of the genetic material. When a species has been identified as a target for gene resource conservation, the objective will, generally speaking, be to conserve as much of the genetic variation as practically possible.

BOX 1. TERMINOLOGY

The terminology used in this note is in accordance with article 2 of the Convention on Biological Diversity (cf. e.g. Glowka et al. 1994). Major concepts used are:

> *'Biological diversity'* means the variability among living organisms from all sources including inter alia terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems.
>
> *'Ecosystem'* means a dynamic complex of plant, animal and micro-organism communities and their non-living environment interacting as a functional unit.
>
> *'In situ conditions*' means conditions where genetic resources exist within ecosystems and natural habitats, and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties.
>
> *'In situ conservation*' means the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties.
>
> *'Ex situ conservation'* means the conservation of components of biological diversity outside their natural habitats.
>
> *'Genetic material*' means any material of plant, animal, microbial or other origin containing functions of heredity.
>
> '*Genetic resources*' means genetic material of actual or potential value.

Genetic diversity or variation is not explicitly defined in the Convention. Genetic variation includes genetic differences between species and within species. The genetic diversity of a species can be divided into inter-population diversity and intra-population diversity, and further into the diversity within an individual expressed by differences between alleles in the two chromosomes of diploid organisms (degree of individual heterozygosity).

The value of genetic variation can be expressed as an ecological, economical or ethical value. In practice, however, it is difficult to determine whether a specific genetic variant of a species will be of future value. Hence, within species it is difficult to separate the 'resource' from the rest of the variation and in reality it is impossible to distinguish between genetic resources and genetic variation (Graudal *et al.* 1995).

Conservation of a resource is here understood as measures that assure its continued existence and availability (FAO 1989, cf. also Glowka *et al.* 1994 and the World Conservation Strategy 1980 (IUCN) *et al.* 1981)).

The concept of resource in a narrow sense of being something useful (to human society) is thus not entirely applicable to the gene level, because in principle all genes are considered potentially useful. The resource referred to in gene resource conservation is therefore really identified at the species and population level. Considering the thousands of species and their distribution in an even more numerous number of populations, critical issues in gene conservation planning are therefore how to identify the group of target species to be included and how to select the populations to be conserved (Graudal *et al.* 1995). These issues are discussed in section 2, 4 and 5.

In order to conserve the genetic variation of a species adequately, the variation should ideally be known. For most species, our knowledge of their genetic variation is still minimal. The central dilemma of gene resource conservation is a recognised need of conservation without knowing exactly what to conserve. The genetic variation will to a large extent have to be 'guessed' based on ecological factors. Assessment of genetic variation is dealt with in section 3.

1.4 Conservation methods

The principles of conservation of genetic variation are the same for all living organisms. The conservation methods will, however, vary according to the specific objectives of conservation, and the distribution and biological nature of the material to be conserved (FAO 1989). The term 'method' is often used to denote different concepts: *in situ* conservation, *ex situ* conservation, ecosystem conservation, species conservation, conservation of intraspecific variation, evolutionary conservation, static conservation, selective conservation, conservation in use, and possibly more.

Here we prefer to distinguish between two basically different methods of conserving genetic resources: evolutionary conservation and static conservation (Guldager 1975); whereas ecosystems, species, populations and individuals are considered objects for conservation (cf. section 6.1). The concepts of evolutionary and static conservation introduced by Guldager (1975) correspond to the more commonly quoted differentiation of conservation and preservation made by Frankel and Soulé (1981). Evolutionary conservation is also denoted dynamic conservation (Frankel and Soulé 1981, Eriksson *et al.* 1993).

Evolutionary conservation is done in living populations, *in situ* or *ex situ* - cf. e.g. FAO (1989) or Keiding and Graudal (1989). In such populations, the genetic composition of target species is allowed to adapt to the prevailing environmental conditions and their change with time. Climatic changes at a given site may thus be responded to by corresponding adaptation of the local conservation populations to the new conditions through natural selection in favour of the fittest trees.

Static conservation maintains specific genetic compositions, e.g. in the form of seed lots or gametes in long term storage in gene banks or vegetatively propagated clones (cultivars) in clone collections, and will usually be *ex situ*, but can also be *in situ* (e.g. species propagating vegetatively in nature). Well defined genetic material can thus be conserved with their present genetic composition as no changes - in principle - should take place in static conservation.

'Conservation in use', i.e. conservation of genetic variation through existing silvicultural management practices, will typically be selective and evolutionary, but can also be static. Regeneration of target species based on natural seed fall will thus contribute to conservation of the genetic resources, because the local gene pool is used in subsequent generations. Selective thinning will often support natural selection because the most healthy trees are favoured - conservation will thus be evolutionary. Systematic thinning on the other hand will at least to some extent maintain the existing genetic composition and therefore contribute to static conservation. Ultimate static conservation is the consequent use of specific clones; but even in clonal forestry this is seldomly the case, as new clones are continuously brought in.

The genetic resource areas (GRA's) used for *in situ* conservation in Malaysia (Tsai and Yaun 1995) are based on a kind of 'conservation in use'. A part of the managed forest area is assigned for gene

resource conservation. Timber is still extracted from these areas, but with more restrictions on target species than normal logging practices: a high number of individuals should be left of the target species, and stricter cutting limits are applied.

Conservation of genetic resources in the production systems sounds, and is to a certain extent, very appealing (cf. e.g. Kanowski and Boshier 1997). A popular notion of this concept has been formulated by Gamez: 'use it or lose it!' (Allegretti et al. 1996). Such integration of conservation and utilisation will often have the scope of being effective. There are, however, important exceptions. Widespread use of few highly bred strains is for instance known to be at the expense of local varieties in agriculture. In forestry, uncontrolled and undocumented movement of tree seed is a serious threat to the maintenance of genetic identity of local populations. Use in itself may therefore in some cases pose a threat to the possible use of some resources in the future.

Conservation of genetic resources generally requires simultaneous use of several methods. Conservation methods are discussed in more detail in section 6 and practical management guidelines in section 8.

1.5 Organisation, target groups and stakeholders

Objectives of conservation normally refer to the benefits of present and future generations. The derived benefits of using appropriate genetic material in forestry touch upon many parts of society. Areas where genetic resources of common interest occur may be owned and at present used by different individuals, communities or public organisations. Interests involved in forest genetic resources are generally many and organisation of conservation may therefore be complex.

Furthermore, the distribution of species and ecosystems do not respect national boundaries. Conservation of genetic resources in one country may often be to the benefit of other countries, where the species are grown or have future potential. The potential benefit of international co-operation between national programmes for conservation of genetic resources is thus quite obvious. Nevertheless it is from a practical point of view necessary initially to adopt a national approach, as a basis for international collaboration.

An important question to consider in planning genetic resource conservation is the national organisation. Who is going to do what? Different units and administrative bodies with vested interests may typically already exist, e.g. a Tree Seed Centre, a Forest Service, a Forest Research Institute, a National Parks Service, and an Agricultural Extension Service. Private sector interests, whether commercial, subsistence or non-profit, may also be present, often in particular where other conservation efforts are already in place or where large afforestation programmes operate. Such existing organisational structures will usually have important roles to play.

Planning should consider the distribution of tasks among existing units, identify the need of possible new units or structures in particular concerning responsibilities and activities at the different administrative levels of the country. In this context it is important to know the different stakeholders, their possible organisation and economic capacity.

Direct beneficiaries are groups and individuals involved in using the forests or in tree planting. Owners and users of the land will obtain a higher or an improved yield of products and other benefits of forest lands - and in particular of tree planting - by using the best available genetic resources. Different types of stakeholders can e.g. be government authorities, state enterprises, private companies, non-governmental organisations (NGO's) and individual farmers. They will often represent different types of interests.

The government authorities - usually the ministry of environment, the forest service or the like - will in principle typically represent the long-term interests in conserving the genetic resources and the biological diversity, and in maintaining the vegetative cover for environmental protection purposes. State enterprises and private companies will typically have a direct commercial interest in improved wood production, which is also of a national economic interest, both through a

reduction of import requirements and through the generation of jobs in the sector itself and in derived sectors. The interests of farmers may be commercial or for subsistence, whether in terms of wood fuel, small timber, fodder, food, shelter or environmental protection. NGO's may have similar interests, but will in addition often represent more ideal objectives of nature conservation, i.e. focus more on intrinsic values.

Organisation and implementation planning is discussed further in section 7.

1.6 Conservation planning

In summary, planning of conservation of genetic resources involves:

- setting of priorities, i.e. identification of genetic resources of priority, usually at the species level based on their socio-economic value (section 2),
- assessment of the genetic variation of priority species, which for most species will have to be based on genecological zonation (section 3),
- assessment of conservation status of target species and their populations (section 4),
- identification of conservation requirements, typically at the population level, i.e. identifying geographical distribution and number of populations to be conserved (section 5),
- identification of appropriate conservation methods - biological and economic options (section 6),
- organisation and implementation planning (section 7), and
- provision of management guidelines (section 8).

2. Setting priorities: selection of target species

The identification of genetic resources of priority is a cost/benefit consideration. Species, cultivated or wild, that have present or potential value to human society will usually merit more intensive conservation than species without such apparent value. Natural populations of Tectona grandis or Acacia senegal will e.g. be given high priority due to their known economic importance. For non-marketed species or species used in subsistence economy, their priority are harder to define. Species with only modest present utility value - e.g. rare, but high value timber species, logged occasionally in natural forest - may have a large potential and must therefore not be forgotten in the process of setting priorities.

The conservation status of species and their populations is a second major factor to consider. The conservation status itself may be used as an indicator for prioritisation - this is often done in species conservation programmes (the 'Red Data Book' type of approach - cf. e.g. IUCN 1978).

Within the context of genetic resource conservation, present or potential utility is assessed first, and then the conservation status in order to identify conservation options and required conservation intensity. If the conservation status is good, there is no need for further action. It is often species with only little present use that have the poorest conservation status. Assessment of conservation status is dealt with in section 4.

At the international level, priorities in forest genetic resources have regularly been identified by the FAO Panel of Experts on Forest Genetic Resources (FAO 1969-1996). Priorities are given by geographical region, species and operation. The priority of species is defined in different end use categories, which provide an indication of their socio-economic value. Priorities for action for each species are given in the logical sequence of exploration/collection, evaluation, conservation and utilisation of the genetic resources. Such prioritisation may provide inspiration and guidance at the national level.

Efforts should also be taken to conserve endangered species, even if they are seen as having little or no utilisation value. However, conservation of such species will typically be integrated in more general nature conservation activities outside the framework of specific gene resource conservation programmes.

For the purpose of *in situ* conservation of genetic resources in Cameroon, three groups of target species were identified (Letouzey, Vivien and Satabie 1984): (i) species heavily utilised for industrial wood, for food, fodder, fuel, or other purposes (20 species), (ii) species considered rare, vulnerable, or endangered (58 species), and (iii) species currently subject to felling control (40 species). Species from the first two groups were considered of most immediate priority due to the complete lack of protection (Graudal 1987).

2.1 Assessment of the present and future socio-economic value of species

The value of species in present use can be assessed in different ways. Their use in planting programmes is one indicator. A better estimate may be obtained by calculating total value production based on planting programmes and market values of the products. Knowledge of consumption patterns through market surveys may provide information on species that are harvested in natural forests. These methods may typically be used for plantation species and for marketed species. For species with products not frequently marketed, user-preference investigations may be required (Franzel et al. 1996, Warner 1995, Lillesøe and Kaumi 1993, Aalbæk 1994).

For highly valued and commercialised species, information is often relatively easily available and their priority in genetic resource conservation programmes consequently easy to assess.

Detailed information is e.g. available on the value production of teak (Tectona grandis). The utilisation value of teak in Thailand can therefore be derived from the expected size of future plantation programmes. Kjær and Foster (1996) have compiled such background data and estimate the yearly value production of the teak plantations on suitable sites to be more than 7000 US $ per ha. Using these data, Kjær and Suangtho (1997) could estimate the yearly value production of the teak plantations in Thailand and the expected gain from using genetically good seed sources.

For most species the process of identifying their priority is more laborious, because data is not available to the same extent. It may also be difficult to compare marketed and non-marketed species.

There are three different ways of assessing priority:

- Survey of area and value production in planting programmes
- Market survey of forest products consumption
- User preference measurements

The two first methods are in principle simple, whereas the third is often more complicated. Preference measurements may also reveal priorities, which are otherwise undetected, due to lack of availability, e.g. because the species have disappeared.

In table 2.1 is given an example of ranking of species in order of priority in the Sudan using the three different methods. The three main columns in the table are not directly comparable, but they all provide important information related to species priorities. The planting figures cover the whole of Northern Sudan estimated by the central government forest authorities (FNC 1993/94, here according to TSP/DFSC 1996). In planting programmes it is seen that ranking changes, when multiplying planting area with value production. A recent ambitious forest products consumption survey in the Northern Sudan (FNC/FAO 1995) includes information on the value of non-wood forest products at species level. Although only some forest products are represented, it is interesting to note that some species primarily harvested in natural forest are high ranking. The user preference measurement shown represents only a very small sample (Pretty and Scoones 1989), but provides the important indication that preferences at the local level may differ considerably from prevailing planting programmes.

Whenever possible, the three approaches, (i) surveys of value production from plantation programmes, (ii) market surveys of consumption, and (iii) user preference studies, should be combined to give a realistic and fully valid impression of species priorities. It is especially important

to examine carefully the potential of highly valuable species, which may contribute only little to the economy simply because they are rare. Also, the value of locally used species, which are not traded at high prices on international markets, should not be underestimated. Such species may be of major importance for the subsistence of local populations in rural areas.

Table 2.1 Ranking of species in order of priority in the Sudan based on present planting figures (1993/94), consumption of non-wood forest products (1993/94) and preference measurement in two villages (1989). Figures in bold indicate priority 1 and 2 in respective cases. See the text for further explanation. Sources: FNC 1993/94 ([1]TSP/DFSC 1996 (Table 5.1 and 5.2), [2]FNC/FAO 1995 (Table 4.2 and 4.3), [3]Pretty and Scoones 1989 (figure 25B and 29a-c).

Species	Central national survey of planting programmes[1]				Market survey of non-wood forest products[2]				Preference measurement in two villages, ranking only[3]	
	Area		Value production		Export		Home consumption			
	Rel. value	Rank	Rel. value	Rank	Rel. value	Rank	Rel. value	Rank	Faki Hashi, Khartoum	Sheik el Siddiq, Blue Nile
Acacia senegal	100	1	100	1	100	1	-	-	-	-
Eucalyptus sp.	20	2	50	3	-	-	-	-	6	-
Acacia seyal	10	3	2	6	-	-	-	-	3	-
Other thorny (i.a. Prosopis juliflora, Acacia tortilis)	9	4	58	2	-	-	-	-	-	1
Other non thorny (i.a. Neem, Dalbergia)	3	5	32	4	-	-	-	-	1	-
Balanites aegyptiaca	2	6	12	5	-	-	21	6	-	6
Acacia mellifera	1	7	1	8	-	-	-	-	-	5
Acacia nilotica	< 1	8	1	7	-	-	1	10	2	2
Ziziphus spina-cristii	-		-	-	-	-	26	4	4	4
Faidherbia albida	-	-	-	-	-	-	-	-	5	3
Acacia nubica	-	-	-	-	-	-	-	-	-	7
Boswellia papyrifera	-	-	-	-	1	4	17	7	-	-
Adansonia digitata	-	-	-	-	0	6	54	2	-	-
Tamarindus indica	-	-	-	-	1	5	100	1	-	-
Hyphaena thebaica	-	-	-	-	-	-	26	5	-	-
Lawsonia inermis	-	-	-	-	8	2	31	3	-	-
Cassia senna	-	-	-	-	1	3	2	9	-	-
Grewia spp.	-	-	-	-	-	-	6	8	-	-

3. Assessing genetic/genecological variation

Reliable information on the distribution of genetic variation - within and between geographic regions - is important in order to establish an effective network of conservation stands. All major gene pools should be conserved, but the number of conservation stands should on the other hand be limited to a manageable level.

The genetic variation of a species can be assessed by different techniques. It is possible to study morphological and metric characters in field trials, biochemical and molecular markers in the laboratory, and to guess on possible genetic variation patterns from ecogeographic variation.

3.1 Field trials and genetic markers

The study of metric characters or adaptive traits in field trials was earlier the dominating technique and it is still today the most robust and valid way of assessing genetic variation in these characters. The actual performance is assessed under conditions which is close to the conditions under which the trees grow in plantations. Information from such experiments is very valuable when assessing adaptive genetic variation as a basis for conservation activities. Studies on performance under controlled conditions may be an important supplement.

Bingchao *et al.* (1986) e.g. found - somewhat surprisingly - in green house tests that teak (Tectona grandis) provenances from moist parts of South West India could resist drought better than provenances from semi-moist or dry regions. This result is supported by field trials, where the Moist-Indian provenances were found to be superior to provenances from semi-moist and dry regions - even in field trials located in areas with relative low precipitation (Kjær *et al.* 1995). The high drought resistance of the Moist-Indian provenances is probably a result of their special leaf anatomy (Bingchao and Zhen 1986)

The recent rapid development of biochemical and molecular markers allows fast surveys of genetic variation within and between populations. These techniques are powerful in connection with traditional field trials and ecological surveys (cf. below) but cannot replace them. Biochemical markers in general deal with neutral, rather than adaptive genetic variation (Millar and Westfall 1992, Eriksson 1994b), and important genetic differentiation following divergent natural selection in a few generations may therefore not be detected by the markers. This is supported by the fact that several studies of forest trees have shown larger differentiation between adaptive traits than between biochemical markers (Mouna 1990, Karhu et al. 1996, Yang et al. 1997, Kjær *et al.* 1997). The markers can nevertheless supply important information on likely historic migration patterns, amount of pollen flow, and they are efficient tools for examination of breeding systems of target species. Marker-aided sampling strategies have further been developed to assist in deciding how many samples should be collected in which populations (Brown 1989), or to assign priority to different species (Crozier and Kusmierski 1994).

3.2 Ecogeographic variation and genecological zonation

A total survey of the genetic variation of all species identified for genetic resource conservation is not practical nor economically possible. The study of genetic variation in adaptive traits requires in general that the species should be tested for long periods and at many sites. A survey based on the use of ecological data in combination with biochemical markers and data from already established field trials is probably a possible way to approach the problem for many species within a realistic time span. Such surveys are, however, not possible for all species. For the time being, the required number and the optimal geographic distribution of the conservation stands must be decided by other means.

It is generally assumed that similarity of ecological conditions implies similarity of genetic constitution (Frankel 1970). This is based on the assumption that local adaptation through natural selection is the overriding force in the process of genetic differentiation between populations. A comparison of a species' distribution with well defined ecological zones will thus provide a

framework for sampling of conservation populations. Such ecogeographical surveys have e.g. been used to identify conservation needs for crop relatives (IBPGR 1985a, Hoyt 1988, Maxted et al. 1995), to identify agroecological zones for use of major crops (FAO 1978/80), and to define tree seed zones with specific recommendations for collection (seed procurement zones) and utilisation (seed deployment zones) of seed sources of tree and shrub species (cf. e.g. Barner and Willan 1983, and Buijtenen 1992).

There are many different types of seed zone systems used in different countries, of which the oldest date back from the 1930s (cf. e.g. Ledig 1996). Some examples are Haddock and Sziklai (1966), Barner and Willan (1983), Robbins and Hughes (1983), Campell (1986), Olsen and Aalbæk (1991), Aalbæk (1993), and Aalbæk and Kananji (1995).

For the purpose of gene resource conservation, this type of zonation is referred to as genecological zonation (cf. e.g. Graudal et al. 1995). A genecological zone can be defined as an area with sufficiently uniform ecological conditions to assume similar phenotypic or genetic characters within a species. Such zonation is based on a compromise between the variation in ecological factors and expectations of gene flow. The zones should not be too small, because pollen flow between neighbouring zones would then be likely to prevent that any genetic differences develop between populations from the different zones. On the other hand, the zones should not be too large, because then important genetic differences may exist between populations within each zone.

Compared to seed zones, genecological zones may differ in (at least) one aspect. A seed zone may be composed of a group of geographically similar but separate areas. If the geographic separation may constitute possible barriers to gene flow, such areas should most likely be considered as different genecological zones (see e.g. figure 3.1).

General genecological zonation

Initial genecological zonation will usually have to be prepared as one common system for several species. Factors typically used for zonation are natural vegetation, topography, climate, and soil (see box 2), and barriers to gene flow (see box 3).

Such a system can be based on existing data and maps of vegetation, topography, climate, and (optionally) soil. It will then often correspond fairly closely to existing vegetation classification. An example of a seed zone system from Sudan prepared this way is shown in figure 3.1.

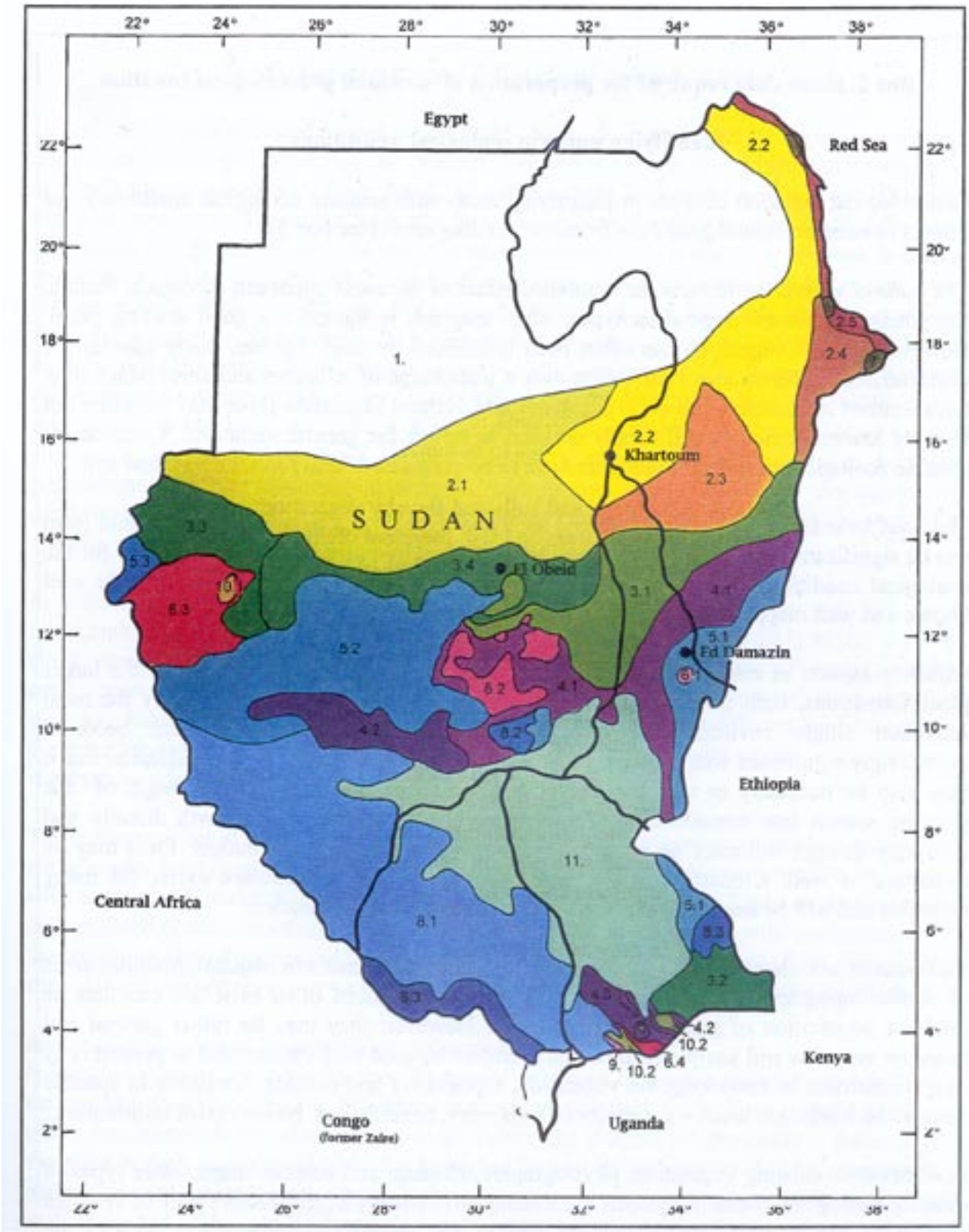

Figure 3.1. Major seed zones in the Sudan (redrawn after Aalbæk and Kanandji 1995). Geographically separate areas of the same seed zone may constitute different genecological zones.

Box 2. Basic data required for preparation of common genecological zonation

Identifying uniform ecological conditions

Genecological zonation consists in identifying areas with uniform ecological conditions and subject to none or limited gene flow from surrounding areas (see box 3).

The *natural vegetation* reflects the combined effect of the most important ecological factors. Knowledge of natural vegetation types, often mapped, is therefore a good starting point. However, natural vegetation has often been influenced by man. Further, many species are characterised by continuous distribution over a wide range of climates and sites, which may have resulted in genetic variation in adaptive traits. Natural vegetation types may therefore not be truly known or not be sufficiently detailed to reflect the genetic variation. A number of specific ecological factors will therefore have to be considered: land form, climate and soil.

The *land form* influences i.a. climate and soils and thereby vegetation: changes in land form can be significant even within small areas and will therefore often be a decisive factor for the ecological conditions. The topography (or physiography) of a country is usually fairly well known and well mapped and therefore an easy factor to use for zonation.

Different aspects of *climate* are the most important factors for the distribution of the larger plant formations, such as forest and woodlands. In lowlands, rainfall is generally the most important single environmental factor, whereas in highlands temperature becomes increasingly significant with altitude. Mean annual rainfall is usually a good indicator, but it may also be necessary to take the annual distribution of the rain and the length of the growing season into consideration. Temperature greatly affects plant growth directly and indirectly through influence on potential evapotranspiration and water budget. Frost may be important as well. Climatic zonation based on rainfall and temperature exists for many countries and will be another important source for genecological zonation.

Variation in *soil* characteristics may cause pronounced differences in vegetation within areas of similar topography and climate. National soil classifications often exist and can thus be used for preparation of genecological zonation. However, they may be rather general and based on very few soil samples and should therefore be used with caution and in general only as a supplement to knowledge on vegetation, topography and climate. Variation in specific features on a regional level, e.g. salinity of soils, may, nevertheless be important information.

In addition to existing vegetation, physiographic, climatic and edaphic maps, other types of existing ecological zonation systems combining different ecological factors will be relevant sources of information. Where satellite images and geographic information systems are available, they can be important tools in preparing the genecological zones.

Box 3. Barriers to gene flow and delineation of zones

Genetic differentiation among populations within a species is promoted by three main forces: natural selection, genetic drift, and mutation. Natural selection in a given environment is generally the most important force regarding adaptive traits such as survival and growth under different conditions. The selection works through mortality. Trees with genes coding for poor adaptation to a given site will die, and the frequencies of such genes thus decrease in future generations on the specific site. There are however also forces preventing or delaying differentiation among populations: phenotypic plasitic y (cf. e.g. Eriksson 1994a and 1995). Phenotypic plasticity is the ability of a genotype to maintain a stable phenotype in different environments (Bradshaw 1965). Genotypes with high phenotypic plasitic y are favoured where environmental factors vary a lot. This will tend to diminish population differences, particularly in the long term. Gene flow is of more immediate importance, because local adaptation will be broken down in each generation when genes are intermixed between populations, typically through pollen flow. Major factors of importance for the amount of gene flow are type of geographic distribution and reproduction and distribution biology of a species.

In general, a continuous distribution allows gene flow to take place and may thus indicate a fairly high degree of similarity among populations. Adaptational forces will typically develop clinal variation following topographic and/or climatic gradients. Sampling of populations for gene conservation may thus be limited to cover a fairly rough pattern of ecogeographic variation. Strongly fragmented distribution and/or occurrence in many different habitats may on the other hand result in more complex genetic patterns that will normally require relatively more stands to be selected in order to sample the genetic variation.

The mating system of a species influences the distribution of the genetic variation. Outbreeders are generally less geographically variable than self-fertilising (autogamous) species, or species with apomixis (Hamrick and Godt 1990). Insect pollinated species are likely to develop more differentiated populations than wind pollinated species due to interaction with the behaviour of the pollinator. Seed dispersal, which depends on the interaction between seed (form, weight, and survival) and seed dispersal vector (water/wind/soil/animals/humans), is of similar importance.

Implications for the use of genecological zonation
If zonation systems are made for specific species or groups of species with similar behaviour, the zonation should account for differences in expected gene flow. In the more realistic situation, where one common zonation system is available, the number of populations selected for sampling in each zone should typically be higher for species with scattered distribution, insect pollination and limited seed dispersal than for species with continuous distribution, wind pollination and wide seed dispersal. Generally, expectations of gene flow tend to reduce the number of zones that can be defined based on ecological factors, as selective differences due to environmental heterogeneity can only result in local adaptation if there are sufficient barriers to gene flow, i.e. differences in ecological factors will result in different zones only if the exchange of genetic material is expected to be limited.

Species-specific zonation systems

The different target species in a given gene resource conservation programme may differ in several ways. They may have different reproduction biology, they may react differently to environmental clines or heterogeneity, and they may reflect entirely different life histories in terms of migration, hybridisation events, or human utilisation. The zonation should therefore ideally be specific for individual species, or at least for major groups of species. For economic reasons - and due to lack of species specific data - such specific systems will in general be limited to species of major importance. Species-specific zonation will require the same basic data as the common zonation. In addition, the distribution of the species should be mapped, and its reproductive and distribution biology should be considered (see box 3). If results from field tests and studies of genetic markers are available, they should be used as well (cf. below).

A species specific genecological zonation has been suggested for teak (Tectona grandis) in Thailand (figure 3.3) by Graudal et al. (in prep.). Teak has a large natural distribution area in South East Asia (figure 4.1). In Thailand, it is found in the Northern part of the country (figure 4.2).

The proposed zonation system for teak in Thailand is based primarily on climate and topography. The climatic tree seed zones constructed by Kaosa-ard (1983), using the ratio between annual precipitation and average temperature is shown in figure 3.2, where the major topographical features are given as well (Mahapol 1954, Royal Thai Survey Department 1978-1995). Teak is not found above 1000 meters altitude and many North-South heading mountain ridges therefore creates North-South heading gabs in the natural distribution of teak in parts of Northern Thailand (see figure 4.2). Data from provenance trials were available, and analysed by multivariate statistics in order to look for 'clustering' between the provenances (Kjær et al. 1996). The result of these analyses revealed a tendency to differences between eastern and western provenances (Kjær et al. 1996 and Kjær (unpublished data)), which may be a result of the North-South heading barriers to gene flow. By further examining the natural vegetation (RFD 1962, 1983, 1993 and 1995, Smitinand 1977, Collins et al. 1991, Boontawee et al. 1995), a total of five genecological zones were drawn (figure 3.3). Further division may be relevant. There are other mountain ridges than the ones taken into consideration here (cf. Mahapol 1954 and Royal Thai Survey Department 1978-1995). Variation in soil characteristics is also present, in particular in zone GV, where the soil in the Southern part is more fertile than in the North (cf. e.g. Mooremann and Rojanasoonthon, 1968). The procedure of establishing the genecological zones is described in more detail by Graudal *et al.* (in prep.).

Revision of the zonation

Genecological zonation is not something fixed, but subject to continuous revision through an iterative, dynamic process as more information becomes available. The validity of an initial zonation can be tested and adjusted as appropriate by classification of environments based on field trials with special emphasis on adaptive traits (cf. e.g. Campbell 1986, Wellendorf 1992, Westfall 1992), and by allozyme studies of the variation for selected species within and between the zones (Millar and Westfall 1992). Use of information from field trials and genetic-marker studies are briefly described in box 4.

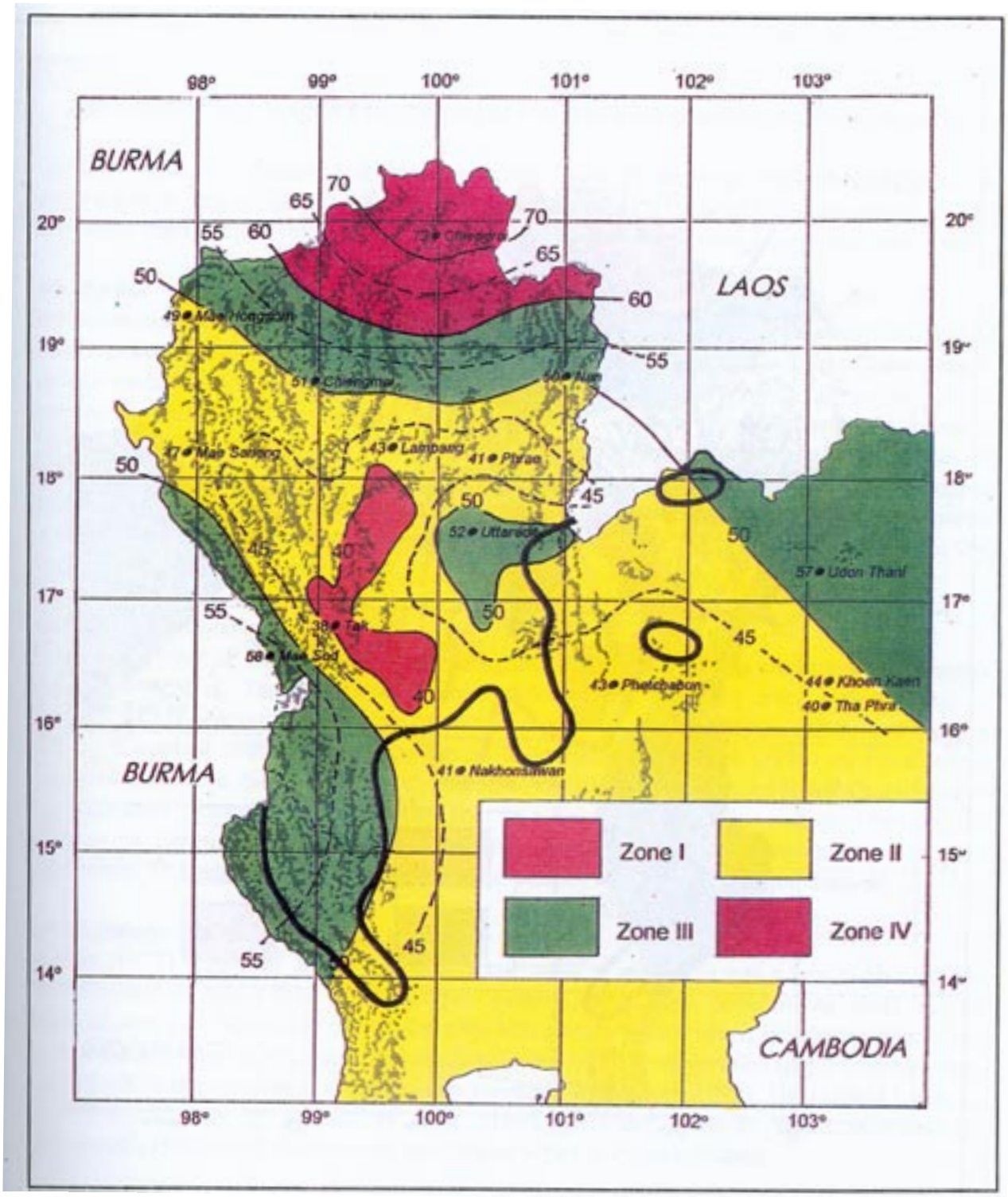

Figure 3.2 Climatic seed zones (Kaosa-ard 1983) and topography (Mahapol 1954) in Northern Thailand. Figures indicate temperature/precipitation ratio. The bold lines indicate the natural distribution limits of teak in Thailand according to Mahapol (1954). Sources: Kaosa-ard (1983) and Mahapol (1954), here reproduced after Graudal *et al.* (in prep.).

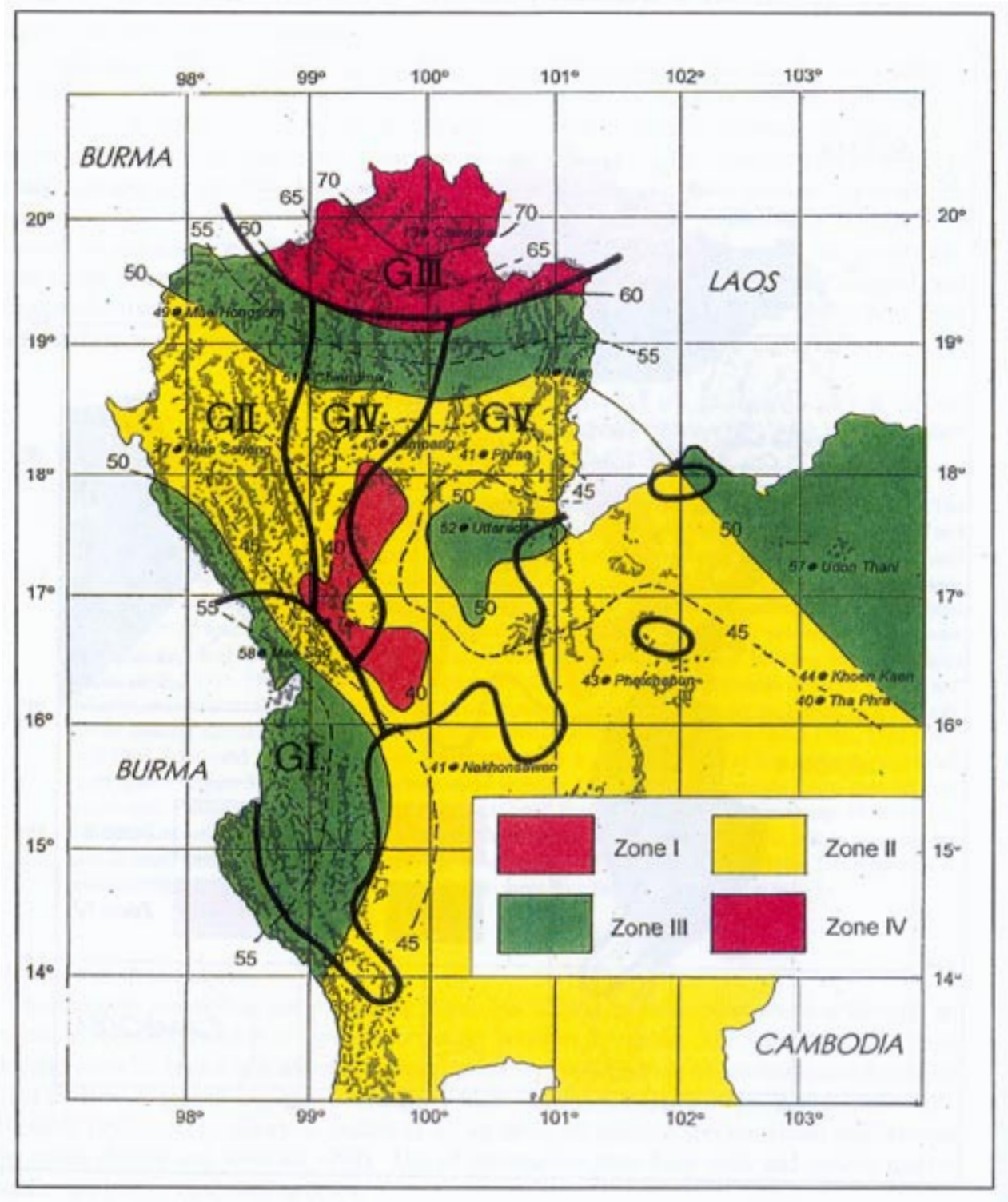

Figure 3.3 Preliminary genecological zones GI - GV for teak (Tectona grandis) in Thailand (Graudal et al. in prep.). The bold lines indicate the natural distribution limits of teak in Thailand according to Mahapol (1954).

Box 4. Use of information from field trials and studies of genetic markers for zonation

Besides evaluation of ecological factors (see box 2 and 3), there are basically three different approaches to genecological zonation. Two of these are based on field trials and one on studies of genetic markers.

Field trials
Evaluation of provenances or other genetic units (families, genotypes) is the traditional aim of tree improvement field experiments. Results are usually presented in the form of provenance recommendations for more or less specific site conditions. The field tests may, however, also be used to characterise the environment for the purpose of zonation. Two approaches can be used: (i) classifying the environments of origin or (ii) classifying the environments of the test sites. In both cases, patterns of geographic genetic differentiation in quantitative traits among provenance samples of different geographic origin are examined. Multivariate statistics such as canonical analysis of variance and cluster analysis (Chatfield and Collins, 1981) may prove useful for this purpose.

Classifying environments of origin
Genetic mapping of natural distribution areas has been used to guide seed transfer for many forest tree species. The procedure involves several steps: sampling trees within a region, evaluating their genotypes, describing the variation patterns, and quantifying risk in seed transfer (cf. e.g. Campbell 1986). The method has i.a. been used by Campbell (1986) on Pseudotsuga menziesii in Oregon, where different characters of rangewide family samples were correlated to environmental factors of the collection sites in a few common garden studies. The complex patterns of genetic variation found, however, made straightforward topographic mapping impossible. The result is areas or groups of areas defined by isolines of major character clusters.

Classifying environments of the test sites
Burdon (1977) suggested to use genotype x environment interactions as a tool to characterise the environment rather than the genotypes. Genetic correlations between the same trait at different sites can be used to cluster the sites into groups within which no serious interaction occurs. Such groups of sites may be considered reasonably homogeneous (deployment) zones, each of which requires identical provenance material (Wellendorf 1992). The method has been applied successfully by Wellendorf et al. (1986) on Picea abies in Scandinavia and by Wellendorf (1992) on an international provenance series of Pinus caribaea.

Genetic markers
The use of genetic markers has been reviewed by Haines (1994). Patterns of isozyme variation are most commonly studied (Hamrick 1994). The genetic markers are normally considered not to be influenced by natural selection. Differentiation between populations in terms of genetic markers thus reflect genetic drift (small population sizes, e.g. in connection with founder effects or genetic bottlenecks), limited pollen flow over many generations, and/or difference between populations in their introduction history to a given region. Hybridisation events will also be detected from genetic markers.

Box 4. ...continued

The ratio of genetic diversity among populations to the total genetic diversity (F_{ST}) is a commonly calculated statistic figure. If all investigated populations are genetically identical, then $F_{ST} = 0$. The differentiation estimated by F_{ST} is - under given assumptions - to some extent a measure of gene flow among populations (Hartl and Clark 1989). Low F_{ST} value indicates a large gene flow, large values a restricted gene flow. The F statistics give estimates of the degree of differentiation of populations, but provide no indication of the relationship among individual populations. Therefore several measures of genetic distances have been derived that quantify differences among populations, cf. e.g. Nei (1972). Genetic distances compare differences in allele frequencies between pairs of populations. Grouping of populations based on allele frequencies are commonly used to present the structure between populations graphically in so-called phylogenetic trees. The idea is to divide all the populations investigated into clusters with a high degree of population similarity and the majority of variation between the cluster groups indicating high levels of gene flow within the group and restricted gene flow between the groups. An example of a phylogenetic tree for some populations of teak (Tectona grandis) is shown in figure 3.4.

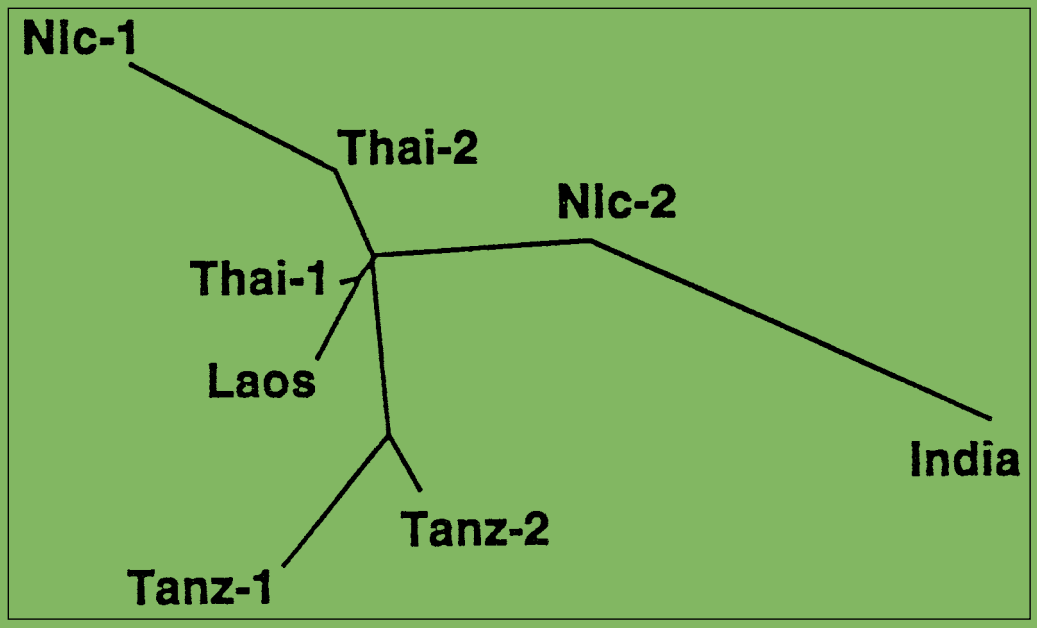

Figure 3.4 An example of a phylogenetic tree comparing four land races of teak (two from Nicaragua (Nic-1 and Nic-2) and two from Tanzania (Tanz-1 and Tanz-2), all four of uncertain origin) with four provenances from the natural distribution area (two from Thailand (Thai-1 and Thai-2), one from Laos and one from India). Branch length in the tree indicate the differences between provenances, but the angles between branches are arbitrary (Felsenstein 1981). The tree indicate that the two Tanzanian land races may be of similar origin, whereas the two Nicaraguan land races seem more different, either due to different origin or due to genetic bottlenecks or hybridisation after introduction to Central America (Source: Kjær and Siegismund 1995).

4 Assessment of conservation status of species and their populations

Conservation status here refers to the present state of the genetic resources and the risk of future erosion of important genetic resources. Questions to examine are: Have populations been lost? How well protected are remaining populations? And have remaining populations been subject to genetic erosion?

Assessment of the conservation status of a species and its populations will have to be based on knowledge of (i) past and present geographical distribution, (ii) prevailing utilisation patterns in terms of direct use in the form of harvesting, planting and breeding of the species (including introduction of intercrossing species/provenances) or indirectly through changing land use patterns, and (iii) its possible occurrence in protected areas.

Geographical distribution

A possible reduction of the natural area of distribution, e.g. due to changes in land use will provide a first indication of the conservation status of the resource. Difference among natural and present distribution may indicate areas of particular attention. The exact geographical distribution of a species is seldomly known. Botanical descriptions and findings will however often enable the preparation of overall distribution maps.

Distribution maps are however often very rough and it may be necessary to specify the distribution e.g. to forest type, altitudinal range or similar to get a sufficiently accurate description. For major forestry species the past and present distribution is often known from regular national forest surveys.

> The natural distribution area of teak is shown in figure 4.1. Teak is generally limited to the mixed deciduous forest in the altitudinal range of 100-900 m a.s.l (Mahapol, 1954; Champion and Seth, 1968), and the distribution area can thus be much better defined than shown in the figure. The distribution of the mixed deciduous forest with teak in Northern Thailand around 1960 (RFD 1962) and around 1990 (RFD 1983, 1993 and 1995, modified according to RFD 1994; cf. also Collins et al. 1991) are compared in figure 4.2. The distribution area around 1960 was much larger than around 1990.
>
> The distribution around 1960 is probably close to the original natural distribution area, although a reduction had taken place already then. It is seen that a large reduction of the natural distribution has taken place since indicating that the conservation status of teak has gradually deteriorated in that area. According to official statistics the total area with natural teak forest in Thailand has been reduced from 65000 km^2 in 1960 to 21000 km^2 in 1990 (Kjær and Suangtho 1997).

Utilisation patterns

For many forestry species, the major threat is conversion of forest habitats to other land uses (cf. e.g. FAO 1993). Such changes will be registered by the reduction of the distribution area. The remaining areas may, however, also be affected.

To get an idea of whether the remaining parts of the natural resource is in a state of genetic erosion, it is necessary to know if, where, and how much it has been subject to selective exploitation.

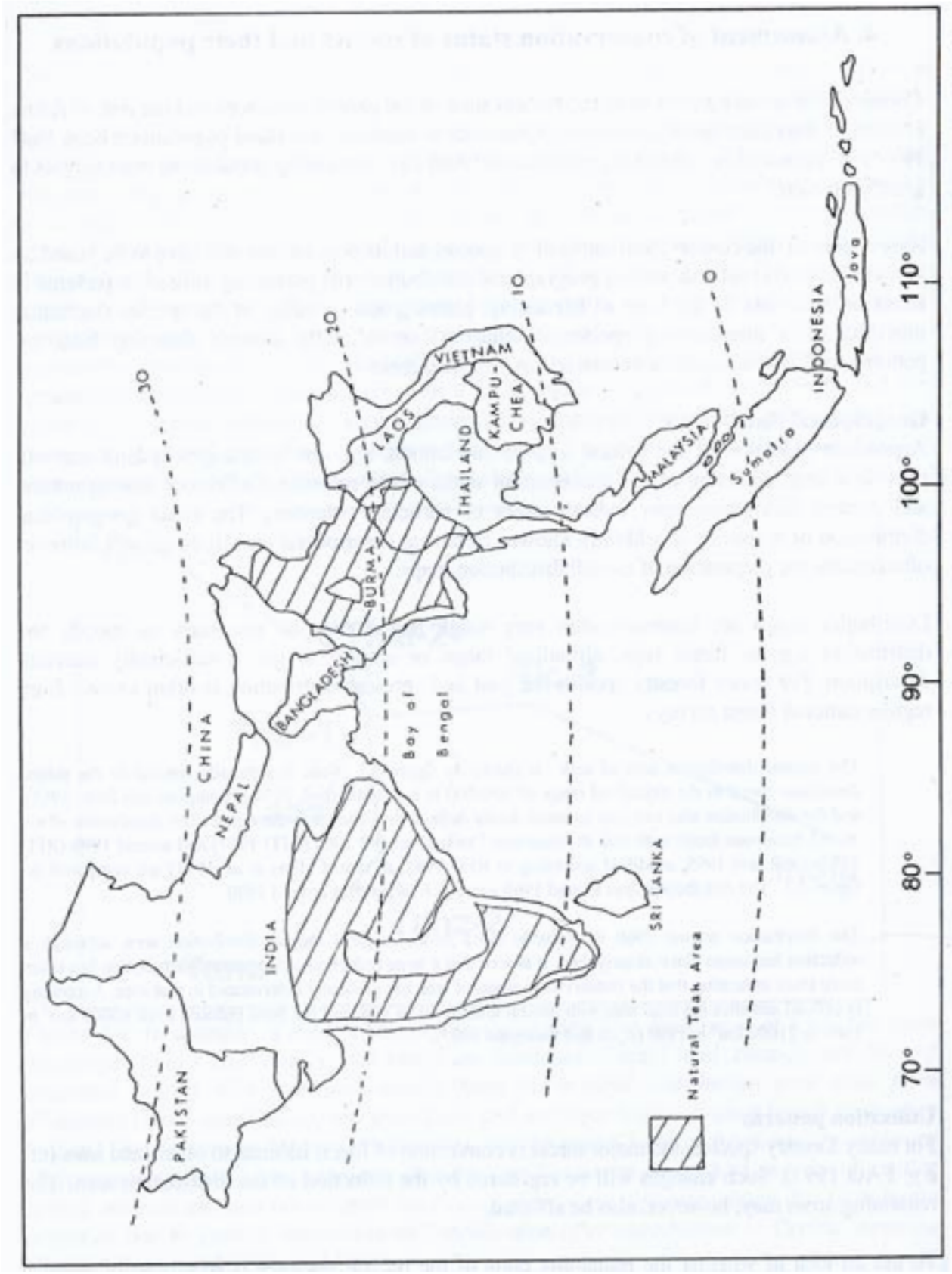

Figure 4.1 The natural distribution of teak (Tectona grandis) (Kaosa-ard 1981, slightly modified according to Champion and Seth 1968 and Keiding *et al.* 1986)

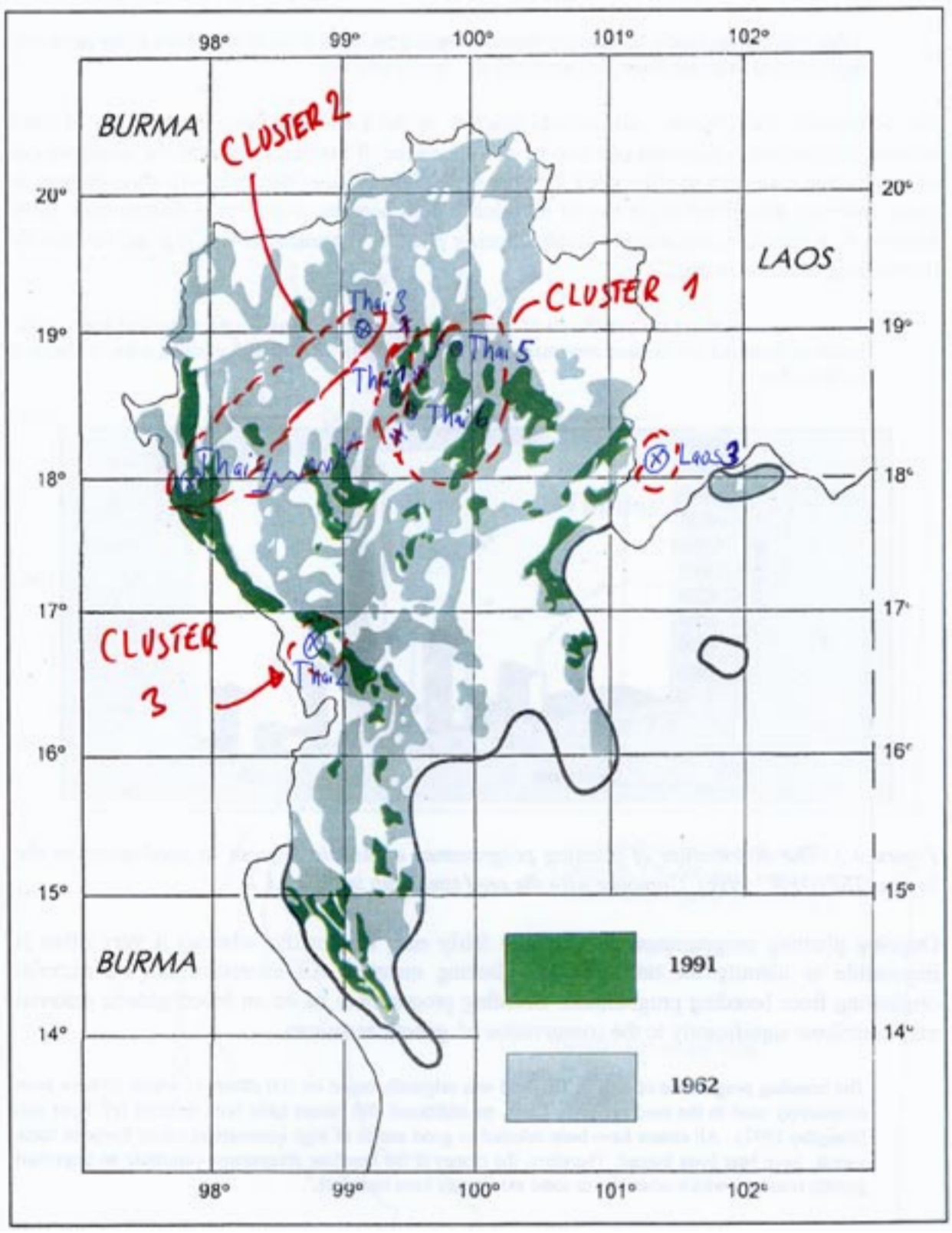

Figure 4.2 Past and present distribution of mixed deciduous forest with teak (Tectona grandis) in Northern Thailand (based on RFD 1962, 1983, 1993, 1994 and 1995, here reproduced after Graudal et al. in prep.).

Again teak may be used as an example. Selective logging has taken place in many parts of the remaining teak forests to an extent where there are hardly any straight trees left.

For commonly used species, silvicultural practice in the form of conscious selection of seed sources for plantation purposes can also be of importance. It may contribute to the conservation of the genetic resources and the need for pure gene conservation measures will then be less. It may, however, also involve the use of introduced seed sources, which may discriminate local sources. It is therefore important to locate ongoing planting programmes and if possible identify the planting material in use.

As examples are shown the distribution of planting programmes of Acacia senegal to seed zones in the Sudan in figure 4.3 (cf. the seed zone map of the Sudan in figure 3.1) and teak planting areas in Thailand in figure 4.4.

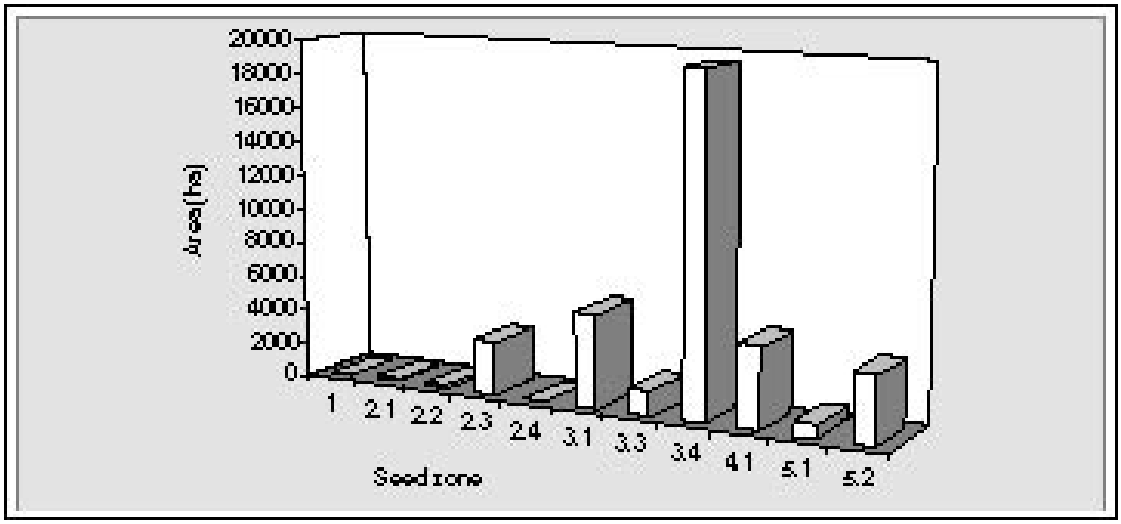

Figure 4.3. The distribution of planting programmes of Acacia senegal to seed zones in the Sudan (TSP/DFSC 1996). Compare with the seed zone map in figure 3.1.

Ongoing planting programmes are generally fairly easy to identify, whereas it very often is impossible to identify the origin of the planting material. An exception can be material originating from breeding programmes. Breeding programmes based on broad genetic material may contribute significantly to the conservation of genetic resources.

The breeding programme of teak in Thailand was originally based on 100 clones of which 60 have been extensively used in the seed orchards. Later, an additional 300 clones have been selected (cf. Kjær and Suangtho 1997). All clones have been selected in good stands of high commercial value. Some of these stands have later been logged. Therefore, the clones in the breeding programme constitute an important genetic resource, which otherwise to some extent may have been lost.

Protected areas

Protected areas have been established in many parts of the world (cf. e.g. Collins *et al.* 1991, Sayer *et al.* 1992, Harcourt *et al.* 1996) and they may often contribute to the conservation of forest genetic resources (Cossalter 1987).

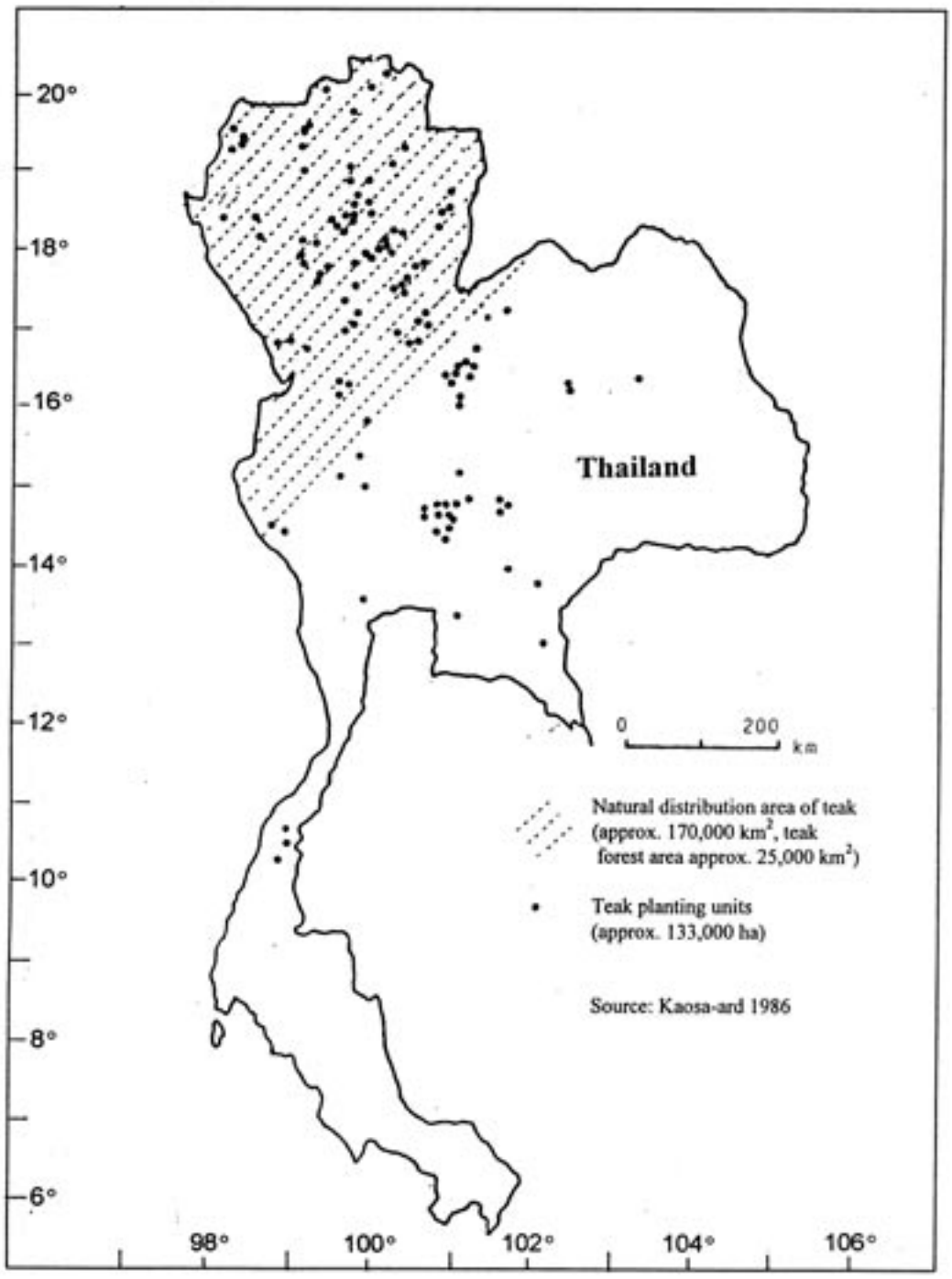

Figure 4.4. Teak planting areas in Thailand (Kaosa-ard 1986).

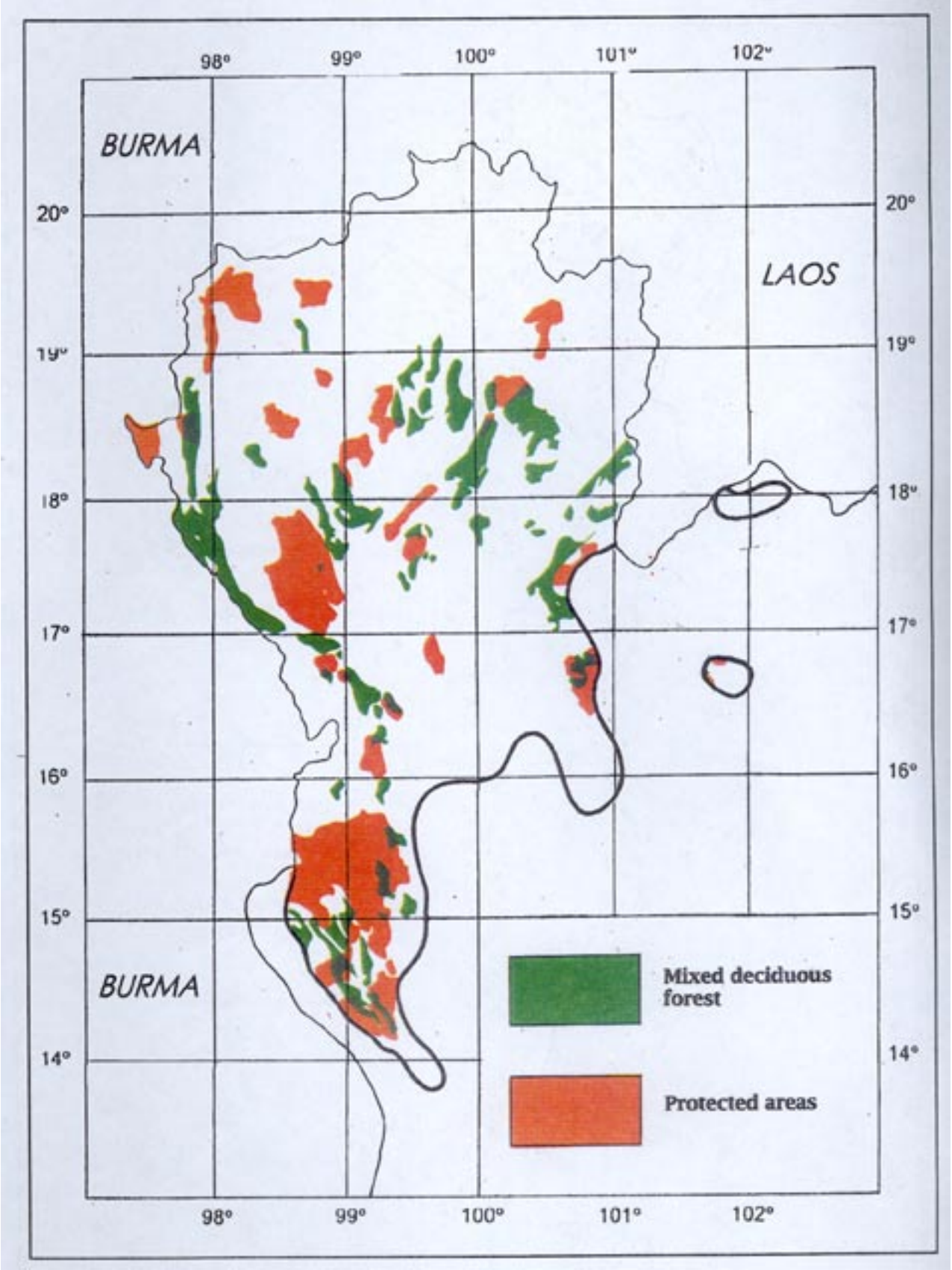

Figure 4.5. Protected areas (Collins *et al.* 1991) and the natural occurrence of mixed deciduous forest with teak in Thailand (RFD 1983, 1993, 1994 and 1995).

Although the occurrence of a target species in protected areas will contribute to its conservation, it is generally not sufficient to capture, in particular the inter-population, variation satisfactorily. Protected areas are often located in remote areas relative to the present and past distribution of the human population. However, unique gene resources may be under severe pressure from conversion of forests to agricultural land, and such stands will typically not be covered by natural reserves if these are located in areas with low human population density.

Tree populations in protected areas may, however, be important elements in a network of conservation populations/samples at a relatively low cost .

An overlay of protected areas with the distribution of teak in Thailand is shown in figure 4.5. In this case there is good opportunity to select conservation stands in already protected areas. It is however also an indication that many resources outside the protected areas probably are lost already (cf. figure 4.2).

The occurrence in protected areas of selected target species for conservation of genetic resources has been investigated in Cameroon (Letouzey 1986). The occurrence of widely distributed species of commercial interest varied a lot. Afzelia bipendensis and Entandrophragma utile was present in 8 of 10 protected areas, whereas Afzelia africana and Triplochiton scleroxylon occurred in only one area and Afrormosia elata possibly in none of the 10 areas (Graudal 1987).

Security requirements

The replication of conservation populations/samples is necessary to minimise the risk of loss due to unforeseen external events (cf. also section 6.1.4). The extent of security requirements necessary should be seen in relation to the factors described above.

5. Identification of populations to be conserved or sampled for conservation

By comparing the genecological zones and the conservation status of a species, it is in principle possible to identify the conservation requirements in terms of the geographical distribution and the number of areas to be sampled for conservation of genetic resources. In practice this comparison will typically consist of several steps:

I. Overlay the genecological zones with:

- The natural (past) and present geographical distribution of the species
- The occurrence of the species in ongoing planting programmes and protected areas
- Location of provenances that are known to be valuable

II. Consider factors affecting the genetic variation, conservation status, and the conservation investment requirements:

- Type of distribution area
- Reproduction and distribution biology
- Differences between past and present distribution
- Size and geographical location of past and ongoing planting programmes, and origin of the planting material used
- Possible effect of selective exploitation in each zone
- Occurrence of populations in protected areas
- Security requirements
- Land tenure and associated options and costs

III. Decide on appropriate geographical distribution and number of areas per zone to be conserved or sampled for conservation of genetic resources.

Overlaying genecological zones and geographically located species information will in practice involve superimposing several different transparent maps: i.a. the genecological zones, species distribution map, maps showing major planting sites and protected areas. The maps will have to be drawn at similar scale, but do not need to be too precise, as the overlay of maps first of all is a planning tool to identify conservation requirements. Computerised geographic information systems (GIS) may be effective tools, if available.

If the genecological zonation is species specific, the type of distribution area and the biology of the species will usually already have been taken into consideration by the zonation. In the more common situation where a general zonation system is available, these factors will influence the number of conservation areas to be sampled in each zone (cf. box 3).

> Stands identified for conservation of teak in Thailand based on the overlay of the genecological zones and the geographical distribution of the species is shown in figure 5.1. Areas identified will eventually have to be verified through field observations.

The overlay described above will provide basis for sampling the genetic variation for genetic resource conservation. Before conservation plans are prepared for the areas identified for sampling, further points of consideration are:

- Conservation options (possible conservation methods)
- Costs of conservation
- Implementation modalities

These subjects are dealt with in more detail in the following sections (6 and 7). Land tenure may influence the choice among areas to sample, where public land often will be easier to access than private. When land areas have been chosen, land tenure will necessarily also influence the choice of the specific conservation measures.

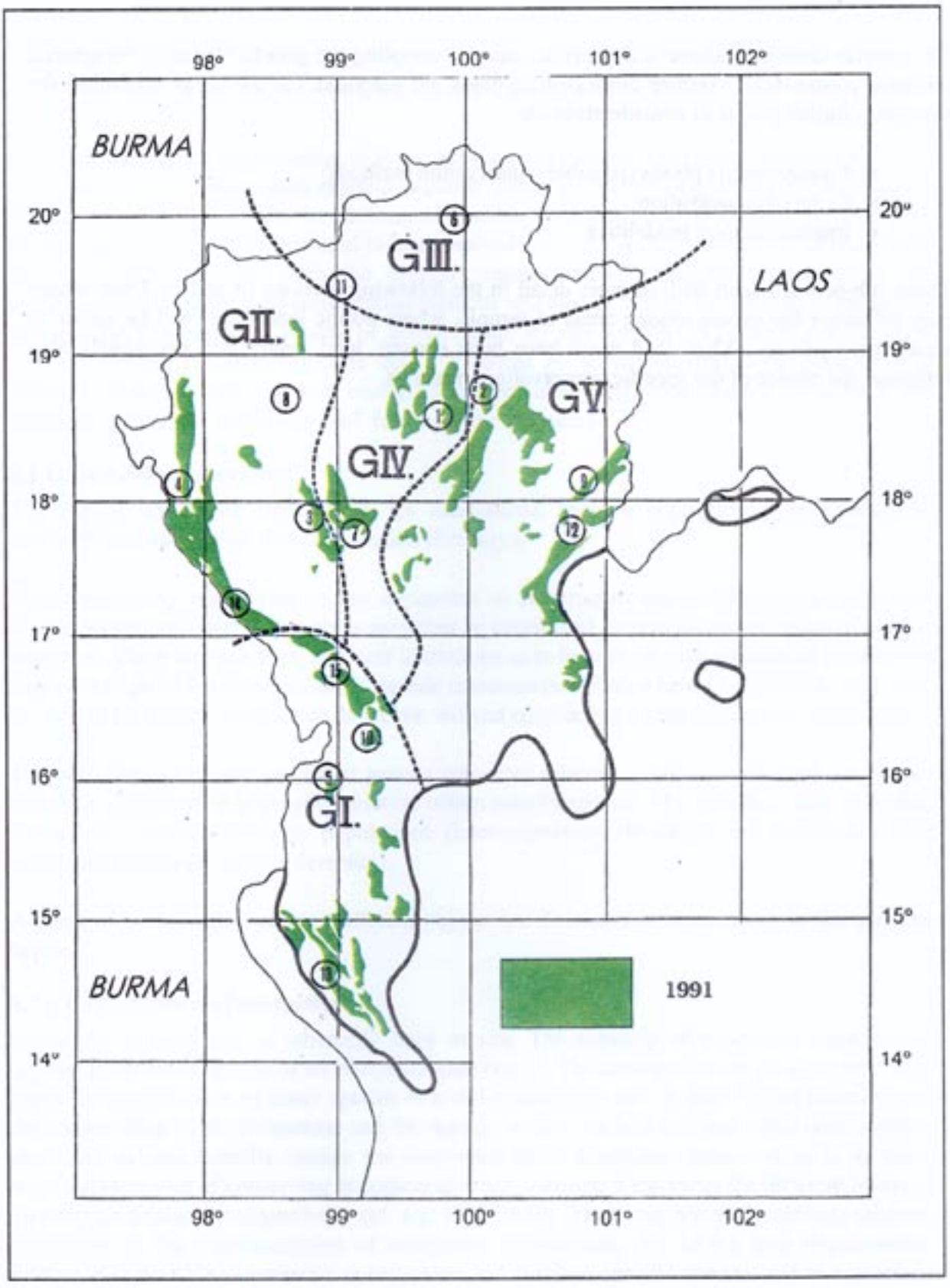

Figure 5.1. Areas preliminarily identified for conservation of the genetic resources of teak in Thailand (Kjær and Suangtho 1997, Graudal *et al.* in prep).

6. Conservation options

Available options for conservation of forest genetic resources are briefly characterised in section 1.4. Selection of conservation method depends primarily on the objectives of conservation. Further, conservation options in the form of possible conservation methods may be limited by the biological nature of the material to be conserved, the socio-economic context of its habitats and the costs associated with the different methods. The feasibility, effectiveness and complementarity of different conservation methods will always have to be assessed in relation to the specific purposes and objects of conservation. In this section, the objects and costs of conservation are described in more detail, followed by an assessment of the feasibility of different methods based on both biological and practical (cost) considerations, leading to the preferred options for conservation of forest genetic resources.

6.1 Objects of conservation

The typical objects of conservation are ecosystems, species, populations (inter-population diversity) and individuals (intra-population diversity).

Most species are, in a varying degree, dependent on the structure and function of the ecosystem of which they are a part. Ecosystems may thus be considered objects for conservation of genetic resources. There are, however, practical limitations as to how much conservation of ecosystems may contribute to the conservation of genetic resources (see further below). Species as such may be objects for conservation, often, however, without considering all the within-species diversity.

The objectives of conserving forest genetic resources referred to above imply that our overall object for conservation is genetic variation within priority species. This variation may be broken down into variation between populations (inter-population diversity) and variation within populations (intra-population diversity).

Aspects of conservation of the different objects are discussed in more detail in the sections below.

6.1.1 Conservation of ecosystems

Ecosystem conservation is inherently done *in situ*. The meaning of ecosystem conservation appears from the definition of an ecosystem (see box 1). The conservation of an ecosystem may imply the conservation of many species in a self-maintaining unit. It may further contribute to the conservation of environmental and life support values, such as soil and water conservation, providing indirect benefits outside the ecosystem itself. Ecosystem conservation is in many ways the ideal way of conserving biological diversity, because it embraces the different levels of diversity and their interdependency (cf. e.g. FAO 1989). There are, however, obvious inherent limitations to the implementation of ecosystem conservation, due to the area requirements. Further, it is possible to conserve an ecosystem and still lose specific species; and to conserve a species and still lose genetically distinct populations, or genes which may be of value for adaptation and future improvement of the species (Wilcox 1982). Some species depend on associated species, while others may require management interventions.

> FAO (1989) quotes an example of Brazil nut (*Bertholletia exelsa*), which has a species-specific pollinator without which it cannot reproduce. Almost all commercial production of Brazil nuts is therefore from wild trees in the natural forest where the pollinator lives. Another example of such interdependency described by Lillesøe (1996) is the flowering patterns of dipterocarps where flowering of certain species occurs in a specific sequence and pollination is done by small weak flying insects. Flowering of some of the commercially most important species happens last in the sequence. As the presence of the pollinating insects depends on the presence of minor species flowering earlier, the reproduction of the commercially interesting species is therefore dependent on these minor species. Traditional thinning used to promote seed production in other species would therefore in this case have the opposite effect.

When conserving a sample of an ecosystem, only part of the intraspecific variation of component species will be conserved. The size and the location of the area sampled will limit the number of populations and individuals representing each species. In practice, conservation of genetic resources therefore goes further than ecosystem conservation (Frankel 1970).

6.1.2 Conservation of species

In the past, conservation generally focused on spectacular species, usually endangered and often of high value. These species were commonly conserved *in situ* in national parks. More recently, *ex situ* facilities have also been deliberately used for species conservation. For animals, *ex situ* facilities include zoo's, game farms, aquaria, and captive breeding programmes (Primack 1993), while plant species can be maintained in botanical gardens and arboreta (Hamann 1992), although botanical gardens often have failed in fulfilling basic requisites for conservation in the past, due to the low number of individuals conserved (Hurka, 1994). Gene banks also conserve species, but will usually have a wider objective of conserving genetic resources within species.

6.1.3 Conservation of inter-population diversity

To conserve the genetic variation of a target species, where genetically different populations have evolved through adaptation to different ecological and environmental conditions, it is necessary to cover the spectrum of ecological variability within the area of distribution of the species (Frankel, 1970). For most species, evolutionary conservation therefore requires a network of living conservation populations: 'conservation in multiple populations' (Namkoong, e.g. 1986, cf. also Eriksson *et al*., 1993). The different stands will be subject to different selection pressures and, thus, with time continue development in different directions. The multiple-population concept will not only be effective in conservation of genetic diversity within species, but can also enhance the total variation by speeding up adaptation to numerous environments. The multiple-population concept in gene resource conservation programmes will resemble the metapopulation structure found in many species under natural conditions (cf. e.g. Nunney and Campbell 1993).

Static conservation of inter-population diversity will similarly require sampling in several populations (Brown and Marshall 1995).

6.1.4 Conservation of intra-population diversity

Evolutionary conservation populations should have a size that reduces the risk of losing genetic variation and avoids built-up of co-ancestry in populations, which may reduce the viability of future generations as a result of inbreeding depression. The size depends on species characteristics and site-specific conservation aspects. Both genetic, environmental and demographic factors are of importance.

Genetic considerations: number of individuals

Conservation populations should not be too small from a genetic point of view. The question of minimum viable population size is central in conservation biology (cf. e.g. Nunney and Campbell 1993). The question may from a genetic point of view be addressed from different angles: (i) to avoid inbreeding, (ii) to conserve a specified proportion of genes with some defined probability, (iii) to conserve evolutionary potential.

To reduce the effect of inbreeding, a conservation population should consist of at least 50 randomly interbreeding individuals (Frankel and Soulé 1981). To conserve most of the genes in a plant population 50 individuals is also sufficient. This will include at least one copy of 95 % of the alleles that occur in the population at frequencies higher than 0.05 (Brown and Marshall 1995).

Although 50 individuals may be sufficient to avoid damage from inbreeding depression and conserve most of the genes, it may still not be sufficient to maintain a large proportion of the genetic variation in the long term. For this purpose, Franklin (1980) suggests conservation populations of 500 individuals. With this size, the in-flux of new variation through polygenic mutations will

be comparable to the loss due to genetic drift (Lande and Barrowclough, 1987). Lande (1995) finds that 5000 individuals, rather than 500, will be required in order to maintain a very high amount of genetic variation in populations. Krusche and Geburek (1991) also recommend larger population sizes, 2000-3000, in order to target rare alleles, as these are not sufficiently protected in populations of 500 individuals. However, rare alleles are hardly of significant importance for adaptive traits under polygenic control, and will therefore often not be targeted in genetic resource conservation programmes (Graudal et al. 1995).

The numbers mentioned above are so called effective population numbers and are calculated based on idealised conditions, which will normally not be valid in natural populations. The effective population size may be much lower than the actual number also called the census number of individuals in populations. This may be due to several factors, e.g. differences in fertility between the individuals, non-random interbreeding, unequal number of males and females in dioecious species, or fluctuating population size from generation to generation (Crow and Denniston 1988).

> The variation in contribution from the parent trees to the next generation has been estimated for Milletia sthulimanii, Brachystegia speciformis, Brachystegia bohemi and Leucaena leucocephala by Bila and Lindgren (1997) in a study from Mozambique. They found that the effective population number was lower than the number of trees in the investigated populations because some trees produce much more seeds than others. The effective population number was estimated to be from 17 to 67 % of number of trees (based on female contribution only), depending on species. A requirement of an effective population number of 50 will thus correspond to approximately 75 to 300 individuals, depending on species.

The basic figures of 50 and 500 (or 5000), should therefore be multiplied with a magnitude of 2-4 and for some species possibly more in order to compensate for the difference between actual and effective population size (Nunney and Campbell 1993, Kjær and Graudal, in prep.).

For evolutionary conservation, we recommend that a conservation population from a genetic point of view should initially consist of at least 150 and preferably more than 500 interbreeding individuals of each of the species to be conserved. In general, the aim should be a final population size of 500-1500. If a larger number of individuals can be maintained at low cost, this should be considered.

> Lawrence and Marshall (1997) are more cautious and suggest a general figure of 5000 individuals. This is, however, based on an example of a herbaceous species, Papaver dubium, where the effective population number has been estimated to be less than 1 % of the census number.

Ex situ conservation of plants normally involves collection of seeds from a number of randomly selected individuals (seed donors) isolated sufficiently by distance to assume that their progenies are unrelated. When seed is collected, collection from 25 unrelated, distant seed donors - which is the internationally recommended practise in forestry - should be sufficient to create a founder population for *ex situ* conservation with an effective population number of 100 (Kjær and Graudal, in prep.).

Environmental and demographic factors

Fires, windthrow or volcanic activity may lead to loss of genetic resources independent of the normal genetic processes. Based on theory and empirical examples, Lande (1988) suggests that unforeseen environmental disturbances or normal environmental or demographic fluctuations usually are of more immediate importance than population genetics in determining the minimum viable size of wild populations.

Demographic fluctuations refer to the variation in population composition (size and sex ratio) over time due to random events in the survival and reproduction of individuals (Shaffer 1981 or

1987). Studies of demography address the same factors as the genetic concept of effective population size (cf. above). Demographic studies, however, consider the development of populations over time, whereas effective population size traditionally refers only to one point in time. The two approaches are also different in their objectives. Demographic studies address the probability of extinction, whereas studies of effective population size address the loss of genetic variation. Time factors can however be taken into account in the concept of effective population size by calculating the aggregated effect over several generations (Crow and Kimura 1970, Orive 1993, Lindgren et al. 1996 and 1997, and Kjær and Graudal, in prep.), which will tend to bring the two approaches closer.

Environmental fluctuations refer both to natural catastrophes, such as floods, fires and droughts, and to normal variation in e.g. climate (cf. Shaffer 1981 or 1987). Environmental fluctuations or natural disturbances of forest ecosystems and their implications for conservation management in general have been reviewed by Attiwill (1994).

Environmental factors are generally extrinsic (external) to the species considered, whereas demographic and genetic factors are intrinsic (internal). Environmental factors, thus, have indirect implications for the number and size of populations required, whereas demographic and genetic factors can be used to estimate the minimum viable size of populations directly. Appropriately applied, demographic and genetic parameters will reflect (past) environmental variation. Possible changes in the future environmental variation patterns, and in particular catastrophic events, are, however, difficult to model and can only be taken fully into consideration by replicating conservation stands.

Combined assessment of the required number of individuals

The minimum viable population size depends on environmental, demographic and genetic factors. So far no model for the combined effect of all factors exists for more general use, indicating that they to some extent will have to be looked at separately.

A species-specific model considering all factors have been developed for the endangered species Banksia cuneata in Australia by Burgman and Lamont (1992).

Lande's (1988) point of view that environment and demography may be of more immediate importance than genetics can be taken into consideration by 'replicating' conservation stands (cf. security requirements, section 4) and by ensuring that conservation populations consist of adequate reproductive and ecological units (Graudal et al. 1995). In a recent review of assessing minimum viable population size, Nunney and Campbell (1993) conclude that demographic and genetic arguments are in surprisingly good agreement in generally putting minimum viable population size at a few thousands adults.

A general conclusion is that there exists no magic figure for minimum viable population size. It depends on the biology of the species and on the options available regarding size, number and location of stands that can be conserved (Nunney and Campbell 1993). Where several (> 2) geographically separate populations of a species are conserved, we consider a population size of 500-1500 adult individuals per managed population a sound general guideline, depending on the ratio between census and effective population number. Unmanaged populations may require larger number of individuals, as the extrinsic factors in such populations will be under no control (Siegismund 1994). The area of a conservation stand required will depend on the density of reproducing trees of the target species.

> In one *Tectona grandis* gene resource conservation stand in Thailand - Mae Yom, see figure 5.1 and table 7.1, the presence of teak was estimated to be approximately 37 reproductive trees per ha in areas of high density (Mahidol University and RFD 1995). Core conservation areas of 4-40 ha should therefore be targeted in order to obtain 150-1500 mature teak trees. In practice, a larger area may be protected in order to assure an appropriate reproduction unit. The generally very low reproduc-

tive success of teak - with large variation in seed yield per tree (Palupi and Owens, 1996, and Tangmitcharoen and Owens, 1996) - may further result in a relatively low level of effective population size compared to other species. More than 150 individuals may thus be required to secure an effective number of 50. This would call for larger areas.

For *Acacia senegal* in Sudan, TSP/DFSC (1996) estimates the normal density of mature trees to be approximately 200 trees per ha in plantations. However, the individuals may be much more scattered in natural populations, where CIDA e.g. found less than two trees (diameter at breast height > 10 cm) per ha in a study in the southern part of the Blue Nile Province (TSP/DFSC 1996). Here, more than 70 ha would be required just to include 150 mature individuals.

A Sudanese *Acacia senegal* tree may on average produce 0.5-1 kg seed, which can yield thousands of seedlings. Acacia plantings with unknown origin may therefore have a low effective population number - independent of their actual size - if all trees originate from seed collected on a few trees. Plantations with unknown origin is therefore not the ideal input to conservation programmes.

The much lower reproductive success in Tectona grandis means that most plantations probably will be based on seed collected from many trees. Still, there may be exceptions - e.g. large parts of all the exotic teak grown in Central America may originate from seeds collected from few trees (Keogh 1980, Kjær and Siegismund 1995).

Theoretical and practical aspects of defining the required number of individuals are discussed by Kjær and Graudal (in prep.) Practical management guidelines are given in more detail in section 8.1.

6.2 Costs of conservation

Conservation of genetic variation is a case of decreasing return relative to population size, because genetic variation is lost proportionally to the inverse of the population size (Crow and Kimura, 1970). As economic resources available to conservation are always limited, one should restrict oneself from investing too much in one species if this means that other species will be neglected, and the number of populations/samples should be limited to be able to monitor and manage them appropriately and securely. At the same time, it should be recalled - as stated above - that species with present or potential value to human society will usually merit more intensive conservation than species without such apparent value. Costs may also decide the choice among conservation options.

The costs of conserving genetic resources can be divided into the following major components:

- Planning and administration of conservation programmes
- Demarcation and management of *in situ* conservation stands
- Establishment and management of *ex situ* conservation stands
- Establishment and management of storage facilities
- Build-up, management and utilisation of collections
- Supportive research and development activities

The costs of the various activities will vary considerably among countries and will have to be calculated based on country specific data. In general terms, the costs will depend on the size of the programme, i.e. number of species, number of populations for each species and the conservation methodology, which from a cost calculation point of view roughly can be divided into two groups:

- establishment of conservation stands and
- collections stored in gene banks.

Planning involves more or less the activities described in this note: (i) identifying priority species, (ii) species specific assessment of conservation requirements, (iii) identification of stands worthy of conservation, (iv) preparation of guidelines for monitoring and management of conservation stands and collections.

Conservation stands are associated with direct and indirect costs. Direct costs of *in situ* conservation stands comprise tending (if any), monitoring and protection. For *ex situ* conservation stands, costs of seed collection, plant production and establishment should be added. Generally speaking, these costs can be estimated based on local experience with resources required for tending, establishment and guarding. Some of these costs may be slightly higher than local standard figures due to the more intensive registration and monitoring of seed and planting stock required.

Indirect costs refer to a possible loss of production value on the area reserved for in or *ex situ* conservation and in a possible isolation zone. Such loss may be difficult to estimate, but will - if relevant - usually have to be based on calculation of internal rates of return or net present values for alternative land use.

The costs of *ex situ* conservation in gene banks comprise establishment and management of infrastructure, development of staff skills, and the build-up, management and utilisation of collections. Build-up and management involves exploration, collection, storage, regeneration, and evaluation of reproductive material; it may also include identification, establishment and management of associated living collections (cf. section 8.2). Costs will vary considerably from one country to another.

> IBPGR (1982) provides estimates of capital and recurrent costs of construction and operation of gene banks for plant genetic resources. Costs are provided at 1981 prices. A revision in 1990 concluded that calculations based on general price inflation would be more than adequate to accommodate for increase in prices, however, varying between countries. The estimates of capital cost for cold room and shelving are between 4 and 1.5 US$ per accession (seedlot) for a capacity of 7,000 to 70,000 accessions and a cold room size range of 50 to 300 m^2. Ancillary facility requirements are estimated to be between 180 and 450 building m^2 at a price of 600 to 1000 US$ per m^2. Equipping the gene bank is estimated to be some 25,000 - 35,000 US$. A model for calculation of running cost of cold room operation at different energy prices is given. Other major capital and running costs which will vary considerably, are costs of regeneration facilities, field collections, extraction, cleaning, establishment and management of field gene banks, and staffing.
>
> The experience of Danida Forest Seed Centre from establishment of national tree seed centres in a number of developing countries (1986-1996) indicates capital costs in the range of 0.5 to 1.5 million US$ and recurrent annual costs in the range of 100,000 to 200,000 US$ (excluding international technical advisors and training). The structure and function of the tree seed centres are similar to the gene bank requirements but have a different objective. Only part of the costs will thus be attributable to purposes of genetic resource conservation alone.

6.3 Feasibility of different conservation methods for different purposes

Advantages and disadvantages of different conservation methods are given e.g. by FAO (1989), Wang *et al.* (1993), NRC (1991a and 1993), Varela and Eriksson (1995), and Eriksson (1994a). They are summarised in table 6.1.

Given the advantages and disadvantages of the different conservation methods, the relative feasibility of different methods for different purposes is summarised in schematic form in table 6.2. The summary is schematic and should not be taken too rigorously. The relative feasibility presented in table 6.2 is based on genetic considerations and the practical limits of implementation (including costs) associated with the different methods (cf. table 6.1 and section 6.1-6.2).

6.4 Preferred options for conservation of forest genetic resources

The preferred approach to conservation of genetic resources in forestry is to maintain evolutionary conservation populations in the form of living stands, preferably *in situ*, but also *ex situ*. In general, *in situ* conservation is the ideal method of conserving genetic resources, especially of wild species.

Table 6.1. Advantages and disadvantages of different genetic resource conservation methods (FAO 1989, Wang et al. 1993, NRC 1991a and 1993, Varela and Eriksson 1995, and Eriksson 1994a).

METHOD	ADVANTAGES	DISADVANTAGES
Evolutionary conservation		
	Allows evolution to take its course, i.e. species to adapt to prevailing environmental conditions and other selection pressures and their change with time. - Applicable to species with orthodox and recalcitrant seeds, and to vegetatively propagated material.	Usually requires much space and resource demanding regulation and protection enforcement. Reconciliation with immediate and basic human needs, e.g. for agricultural land, often difficult.
In situ: Protected areas	- Conserves genetic resources in their natural habitat, maintains interactions with other species and organisms; - Conservation of intra-specific variation can be combined with some degree of conservation of inter-specific variation;	- Large areas required; - Costs of conserving inter-specific variation in general prohibitive; - Resources prone to loss by accident, pests, diseases; - Potential conflicts between different conservation objectives.
In situ: Managed stands	- Conserves genetic resources in their natural habitat, maintains to some degree interactions with other species and organisms; - Conservation of intra-specific variation can be combined with conservation of inter-specific variation through a network of spatially separated areas, which also provide insurance against loss by accident, pests, and diseases;	- Many small areas required; - Knowledge on management interventions needed to meet specified objectives.
Ex situ: Living conservation stands	- Conserves genetic resources in habitats of expected use, maintains to some degree interactions with other species and organisms; - Conservation of intra-population variation can be combined with conservation of inter-population variation through a network of spatially separated areas, which also provide insurance against loss by accident, pests, and diseases;	- Many small areas required; - Spatial isolation to conserve population identity required; - Does not (necessarily) conserve associated species in the ecosystem; - Knowledge of management interventions (including establishment) needed to meet specified objectives. - Relatively expensive (generally not a preferred alternative for species without actual socio-economic value).
Static conservation (*ex situ*)		
	Maintain specific genetic combinations, generally requires less space and is relatively easy to control (less dependent on other land uses).	Often require special facilities and trained personnel and often involve risk of disease transmission. - Does not allow continuos adaptation to changes in the environment. - Does not conserve associated species in the ecosystem;
Seed banks:	- Propagules ready for use; - Relatively inexpensive; little space required (small seeds); - Intra- and inter-population can be conserved provided species range adequately sampled;	- Not applicable to species with recalcitrant seeds nor to vegetatively propagated species; - Space required (large seeds); - Regular regeneration of seedlots may pose problems;

Pollen banks	- Minimum space required; - Applicable to species with orthodox and recalcitrant seeds, and to vegetatively propagated material; - Intra- and inter-population variation can be conserved provided species range adequately sampled;	- Only half the genome conserved; - Tri-cellular pollen storage extremely difficult; - Needs female flowers for conventional propagation; - Propagules not readily available;
Tissue culture banks	- Minimum space required; - Genetic erosion reduced if methods such as cryopreservation are used; - Applicable to species with orthodox and recalcitrant seeds, and to vegetatively propagated material; - Intra- and inter-population variation can be conserved provided species range adequately sampled; - Aseptic conservation (minimises disease risk); - Time required to produce propagules for use is short.	- Sampling problems (representative individuals and within individual); - Protocols are species and at times genotype-specific; - Problems of somaclonal variation and early maturation;
Clonal archives	- Applicable to species with orthodox and recalcitrant seeds, and to vegetatively propagated material; - Intra- and inter-population variation can be conserved provided species range adequately sampled; - Useful method for unique phenotypes/ genotypes (e.g. mutants, variants, sterile types). - Time required to produce propagules for use is short.	- Space required; - Resources prone to loss by accident, pests, diseases; - Relatively expensive (generally not a preferred alternative for genotypes without actual socio-economic value).
Botanical gardens and arboreta	- Applicable to species with orthodox and recalcitrant seeds, and to vegetatively propagated material; - Useful method for unique phenotypes/ genotypes (e.g. mutants, variants, sterile types).	- Space required; - Resources prone to loss by accident, pests, diseases; - Not apt for conservation of inter- and intra- population variation (requires a larger number of individuals than needed to conserve inter-species variation, which is usually the purpose of botanical gardens/arboreta).

To the extent that static conservation is required, it will often be taken care of by breeding programmes. For economic reasons and when security is evaluated, *ex situ* conservation or a combination of *in situ* and *ex situ* methods will usually be considered.

Table 6.2. The relative feasibility of different conservation methods for different purposes (targets of conservation). The feasibility rating is based on advantages and disadvantages summarised in table 6.1.

CONSERVATION METHOD	OBJECT OF CONSERVATION			
	Ecosystem	Species	Inter-population variation	Intra-population variation
Evolutionary conservation				
In situ: Protected areas	****	**	*	**
In situ: Managed Populations		****	****	****
Ex situ: Living conservation populations		***	****	***
Static *ex situ* conservation				
Seed banks: orthodox seed		***	***	***
recalcitrant seed				
Pollen banks		**	**	**
Tissue culture banks		**	**	**
Clonal archives		*	*	**
Botanical gardens and arboreta		**	-	-

FEASIBILITY [ ] Irrelevant *** High * Low
**** Ideal ** Medium - Very low

Ex situ conservation of seed, pollen or tissue in gene banks will often be important complementary activities (Wang *et al.* 1993). However, the long period of time and the large areas required for regeneration, generally make *ex situ* storage less feasible for evolutionary conservation of woody perennials.

This is largely in contrast to agriculture, where conservation of crops usually is done *ex situ*, in seed banks, field banks or in certain cases as tissue culture, although *in situ* conservation also would be highly relevant, in particular for wild relatives of crops and in some cases for land races (NRC 1993). The great advantage of *ex situ* conservation of agricultural crops in seed banks can largely be attributed to the short regeneration time of most crops (annuals) and the relatively high space- and cost-efficiency of storage as well as regeneration.

Seed viability and life history are factors of importance for the choice of conservation method (Brown and Marshall 1995). Only species with true orthodox seeds can be stored for long periods. The storage of pollen, recalcitrant seed, and in vitro culture are only viable as short term measures (Wang et al. 1993). Gene banks are therefore generally synonymous with storage of orthodox seed in seed banks. Alternatives to storing seed are being developed, but are still not applicable for large-scale long-term storage. Concerning opportunities of using biotechnology for conservation of germplasm reference is made to NRC (1993), Wang *et al.* (1993), and Haines (1994).

7. Implementation modalities and planning

When a genetic resource conservation programme is planned, it is important to consider (i) who is going to take care of the programme and who else may be involved at national level, (ii) whether international collaboration is relevant, (iii) what is going to happen in practice (implementation planning), and (iv) if there are any relevant legislative regulating mechanisms.

Appropriate use of forest genetic resources contributes to improved welfare in general. Regulation to promote sustainable management of the genetic resources may therefore be relevant at national as well as at international level. Legal issues have received increased attention in discussions on how best to conserve and use genetic resources, in particular at the international level. Existing legislation will have to be considered but will vary from country to country. The subject is not covered further in this note. For discussions of relevant issues, reference is made to Klemm (1994), Glowka *et al.* (1994) and Co-sponsors (1995).

Stakeholders and organisation of genetic resource conservation programmes are introduced in section 1.5. Some additional details are given in this section.

7.1 Implementation modalities at national level

The objective of conserving forest genetic resources is closely linked to securing a long-term supply of adequate reproductive material. As a consequence of this, the identification, management and monitoring of the network of conservation stands should ideally be integrated with or closely linked to national tree seed programmes.

Conservation of genetic resources will in general need specialised structures with specific requirements both in terms of infrastructure and staff. Requirements depend on the types and amounts of genetic resources to be handled, and the allocation of tasks among collaborating partners. The development of national strategies for conservation and utilisation of forest genetic resources is an important step in defining the most appropriate organisational set-up and the allocation of responsibilities to relevant institutions, whether existing or required new ones (Graudal and Moestrup 1997).

When the organisational set-up is considered, it is important to realise that the core activities of genetic resource conservation are found in the interface of research and practical application, and of national long-term conservation interests and more immediate commercial and/or subsistence interests.

Vesting the responsibility within government departments will - in principle - assure independence of commercial interests. It will, however, be important to establish close links with seed procuring organisations, whether private or government companies. Likewise it will be important to maintain close links with relevant research (breeding) institutions, whether private or public.

For the well-functioning of genetic resource centres, gene banks or tree seed programmes, it is crucial that conservation of genetic resources, breeding, and supply of reproductive material are organised in an integrated manner. Integration is required to avoid overlap, assure exchange of genetic material and know-how, and thus optimise the use of resources in terms of manpower, money and land.

To make it work, development of staff skills is necessary, and an efficient extension service to users of the reproductive material is required.

The organisational requirements for handling of reproductive material differ for different species. In general, base collections (see box 5 in section 8) should be vested within an independent national authority. This does not prevent other organisations from contributing to conservation of genetic resources. The integration of conservation and utilisation is important for any organisation wishing to exist beyond the short-term. The concept of integrating conservation, improvement and seed procurement is the basis of a number of national tree seed programmes.

The structure of such programmes may, however, vary a lot (cf. Graudal and Moestrup 1997) and it is thus not possible to suggest one model for implementation. Major points to consider in relation to the areas identified for conservation are ownership and associated options and costs of administration and management (cf. also section 5).

Ownership may influence both options and costs of conservation. On private land the costs of *in situ* conservation may be prohibitive, in particular if alternative land use is profitable. Public land may be more or less intensively managed. In some cases genetic resource conservation may be considered free of additional cost (if the resources are already protected for other purposes), in other cases it may require more intensified protection or management.

7.2 International collaboration

There are obvious limitations to national gene resource conservation planning. The natural distribution of priority species are seldomly confined by national boundaries. Furthermore, land races may have developed through utilisation and domestication outside the natural distribution area. Ideally international conservation networks are therefore required and the efficiency of national programmes may in general be considerably improved through such international collaboration. International organisations, like FAO and IPGRI, play an important role in establishing such networks.

Several networks have been established in Europe within the framework of the European Forest Genetic Resources Programme (EUFORGEN) co-ordinated by IPGRI. The networks are for specific species, e.g. Picea abies (Turok et al. 1995) and Quercus suber (Frison et al. 1995), or for groups of species, e.g. noble hardwoods (Turok et al. 1996). Similar networks also exist in the tropics. They have typically been established with a broader perspective including domestication as well as conservation of genetic resources, e.g. the FAO co-ordinated International Neem (Azadirachta indica) Network (Thomsen and Souvannavong 1994, Hansen et al. 1996), the FAO Project on Genetic Resources of Arid and Semi-arid Zone Arboreal Species (FAO 1988, Graudal 1995), and the more recent TeakNet (Ko Ko Gui 1995).

7.3 Planning conservation activities in areas identified for conservation

As summarised in section 1.6, conservation planning involves all steps from setting priorities to provision of management guidelines for the conservation areas and collections required. It is extremely important that the identification of conservation requirements does not become a goal in itself. Practical implementation arrangements should therefore be considered all through the planning process.

The logical sequence of activities presented in this note so far is:

- Selection of priority species
- Assessment of their genetic variation
- Assessment of their conservation status
- Identification of populations to be conserved
- Identification of possible conservation measures

The next step is to decide which conservation measures to apply on the specific populations identified for conservation. The types of question to answer are: Should a given population be demarcated and guarded? Should reproductive material be collected and put in store? Or should it be used for establishment of a new plantation? Or should we use some of these measures in combination? Do we have to consider pure conservation populations or can we combine conservation with some form of utilisation, e.g. seed supply?

In table 7.1 and 7.2 are shown two examples based on consideration of these questions.

Table 7.1 is a detailed example for a single species, showing the preliminary conservation plans proposed for the teak areas identified for genetic resource conservation in Thai-

land; and a more overall plan for several species in the Sudan is shown in table 7.2.

Table 7.1 Measures proposed/considered for the conservation of the genetic resources of teak in the areas preliminarily identified in Thailand, cf. figure 5.1 (Kjær and Suangtho 1997, Graudal et al. in prep). * indicate areas to be surveyed. See also figure 3.2 and 3.3.

Location	Area (ha)	Seed zone	Genecological zone	Conservation measures
Existing *in situ* conservation areas				
1. Ban Cham Pui	20	II	GIV	*in situ*
2. Mae Yom National Park	6400	II	GV	*in situ/ex situ*
Proposed new conservation areas				
3. Mae Ping National Park	1000	I	GIV	*in situ*
4. Huay Mae Salab Reserved Forest	*	II	GII	*in situ/ex situ*
5. Umphang Wildlife Sanctuary	*	III	GI	*in situ/ex situ*
6. Pong Salee Botanical Garden	100	IV	GIII	*in situ*
7. Huay Mae Wang Chan	500	I	GI	*in situ/ex situ*
8. Mae Chaem (Doi Cha Ko Huay Ha)	200	II	GII	*in situ*
9. Huay Mae Lao, Ciang Khong	*	III	GV	*in situ/ex situ*
10. Klong Lan and Klong Wang Chao	*	I	GI	*in situ/ex situ*
11. Doi Chiang Dao	*	IV	GIII	*in situ/ex situ*
Additional areas required				
12. Nam Pat Forest Park	20	III	GV	*in situ/ex situ*
13. Si Nakarin, Kanchanaburi	*	III	GI	*in situ/ex situ*
14. Tha Song Yang	*	III	GII	*in situ/ex situ*
15. Klong Wan Chao	*	II	GI	*in situ/ex situ*

The 15 areas proposed/considered in table 7.1 correspond to the 15 locations indicated on figure 5.1. It is seen that for teak in Thailand, establishment of *in situ* conservation stands is generally preferred in all genecological zones. The selected areas at Mae Yom in zone G IV will, however, be prone to flooding due to planned dam building. Establishment of *ex situ* stands with this material may therefore be relevant. For areas still to be surveyed, *ex situ* conservation will have to be considered, in particular for stands outside protected areas. Storage of teak seed is not a preferred option, due to the relatively short viability of the seed.

Table 7.2 Preliminary conservation measures proposed for the conservation of genetic resources of selected priority species in the Sudan, cf. table 2.1 and figue 3.1. See the text. *** highest priority, **prompt action recommended, *action important, but of less urgency.

Species	**Prioritisation**		**Number of zones/ required conservation stands**	**Proposed conservation measures**				
	Rank	**Status**		***In situ* conservation**		***Ex situ* conservation**		
				Seed sources	Conser-vation areas	Seed stands	Conser-vation stands	Seed storage
Acacia senegal	1	V	15-25	***		***		*
Acacia tortilis	2	V	10-20	*	***			**
Acacia nilotica	2	V	10-20	***				*
Acacia seyal	3	V	15-25	*	***			*
Acacia mellifera	3	V	15-25		**			**
Faidherbia albida	2	V	10-20	*	**			*
Prosopis juliflora (E)	2	-	2-5	*		*		*
Eucalyptus spp. (E)	2	-	5-10	**		**		*
Balanites aegyptiaca	1	V	20-30	**		**		*** (M)
Adansonia digitata	2	E	10-20		***		*	*** (M)
Boswellia papyrifera	3	V	5-10		**		**	**
Borassus aethiopium	1	V	5-10		**			***
Khaya senegalensis	1	V	5-10	**	*			***
Dalbergia spp.	1	V	10-15		**		*	*** (M)
Cordia africana	1	E	10-15		***		*	*** (M)
Diospyrus mespiliformis	1	E	10-15		***			***
Azadirachta indica (E)	1	-	2-5	***		**		-
Ziziphus spina-cristii	3	-	15-25	**	**			-
Tamarindus indica	2	V	5-15		**			*
Hyphaena thebaica	2	V	10-20		**			*
Lawsonia inermis (E)	2	-	2-5	**		**		-
Grewia spp.	3	-	5-15		**		*	-

Table 7.2 provides an overview of suggested priorities for conservation of genetic resources of selected species in the Sudan. Species have been selected based on table 2.1 (Rank). The species *Borassus aethiopium, Khaya senegalensis, Dalbergia spp., Cordia africana* and *Diospyrus mespiliformis* listed here belong to the group of other non thorny in table 2.1 and *Ziziphus spina-cristii* to the group of other thorny. Species of exotic origin are marked with an E. Protection status (E: endangered, V: vulnerable) is according to TSP/DFSC (1996). The number of genecological zones of occurrence for each of the native species hasbeen roughly estimated based on the registered occurrence of the species in the different zones according to Aalbæk and Kananji (1995). These numbers reflect the genecological variation of respective species and the conservation requirements in terms of number of populations. Conservation measures have been given priority rating based on the overall priority of the species, their protection status, and the storability of their seed (- : unsuitable for storage, M: medium term storage possible; otherwise long term storage possible). For species of high priority in tree planting programmes a combination of all conservation measures is proposed with emphasis on evolutionary conservation stands, *in situ* as well as *ex situ*. For species of lower priority, *in situ* conservation is preferred and where possible in combination with long-term storage. Medium-term storage (M) can be used as an interim measure. Where pos-

sible, conservation and seed supply are combined. Conservation measures will have to be further detailed for each species as done for teak in Thailand above.

Other practical examples of systematic national genetic resource conservation programmes targeting inter- as well as intra-population diversity can be mentioned: gene pool reserves of Douglas fir (Pseudotsuga menziesii) in Washington and California (Wilson 1990 and Riggs 1990, respectively - cf. also Millar and Westfall 1996), genetic conservation of Quercus suber in Portugal (Varela and Eriksson 1995), conservation of genetic resources of larger numbers of species in Germany (Kleinschmit 1994), Denmark (Graudal et al. 1995) and Austria (Geburek and Mueller 1996).

8. Management guidelines

From a management point of view it is practical to distinguish between two major groups of conservation methods: conservation stands and gene banks. They roughly correspond to the two major methods of evolutionary and static conservation discussed earlier. The feasibility of the two has been dealt with in section 6.3 and 6.4 above. In practice, management of conservation stands may, however, also serve static conservation purposes, and some gene bank management practices may serve evolutionary conservation purposes.

The identification of conservation objects and the sampling considerations described in section 5 and section 6.1.4 are in principle the same for all organisms and independent of the conservation method per se.

In the following are given brief descriptions of the conservation technologies used in practice for forest genetic resources. Only methods feasible for the conservation of inter- and intra-population variation are considered (cf. table 6.2).

8.1 Conservation stands

Conservation stands are of particular relevance for conservation of genetic resources of trees (long-living perennials), cf. section 6.4. The need for management and the specific management interventions required will vary with species and site specific characteristics of each stand. The literature on practical management guidelines at stand level is scarce, in particular for *in situ* conservation. General guidelines are e.g. given by Graudal et al. (1995) and for *ex situ* conservation stands in particular by Willan (1984) and FAO (1985, 1992), and for *in situ* conservation by Roche and Dourojeanni (1984), FAO (1989), NRC (1991a), Hawkes et al. (1997) and Maxted et al. (1997a and 1997b). For *in situ* conservation most of the guidelines are of a fairly general nature. Maxted et al. (1997b) provide, however, a practical model for *in situ* conservation of plant genetic resources.

Practical studies to provide more specific management guidelines for both in and *ex situ* conservation stands of forest genetic resources are underway within the framework of a collaborative programme between institutions in a number of countries, FAO and DFSC.

A conservation stand can consist of one or several species, i.e. either a pure stand or a mixed stand. In a mixed stand, one may target one or several species for gene conservation. The stand can be established artificially (planted or sown), or through regeneration (natural or assisted by silvicultural interventions). Artificially established stands will typically be *ex situ* conservation stands and naturally regenerated stands will often be *in situ*. General management prescriptions for in and *ex situ* conservation stands will often to some extent be the same, but there are differences, in particular between *ex situ* stands to be established and existing *in situ* stands.

The design and management of each stand should be registered in management protocols.
Crucial (more or less) manageable factors for conserving the genetic variation of a stand are:

- size and family structure
- regeneration and isolation
- tending
- utilisation
- site conditions

Both the genetic, demographic, environmental and socio-economic conditions are of importance (cf. section 6.1.4).

Size and family structure

Theoretical aspects of population size are dealt with in section 6.1.4. In practice the size will depend on species and site specific conservation aspects. Mixed stands where the objective is to

conserve the genetic variation of one or more species will in general have to be larger than pure stands.

As a rule of thumb, an *in situ* stand of a wind pollinated species should initially consist of at least 150 and preferably more than 500 interbreeding individuals of each of the species to be conserved. For species naturally occurring in small populations (e.g. adapted to small ecological niches), fewer individuals may be accepted. Depending on the ratio between census and effective population number, final stand size should be 500-1500 individuals or more per species. In particular unmanaged populations, which normally will be *in situ* stands, may require larger numbers (cf. section 6.1.4). Where a population is smaller, this may be achieved by enlarging the population through regeneration on adjacent areas in order to minimise the continued loss of genetic variation in future generations. The size of the area should be large enough to maintain the minimum number of individuals required at generation turn-over.

Seed collection from one species in a stand for the purpose of establishing an *ex situ* stand should involve at least 150 trees if their relationship is unknown. Seed should be collected from at least 25 randomly chosen and supposedly unrelated individuals (i.e. half-sib families). If the individuals in the mother stand are supposedly unrelated (e.g. if the stand is established artificially from seed), the rule of thumb is that it should consist of at least 50 trees. When *ex situ* conservation stands are established, the aim should be a final stand size of 500-1500 individuals or more.

Regeneration and isolation
The conservation stands should be regenerated with genetic material originating from sexual reproduction in the stands and with as little genetic influence from outside in the form of contamination with pollen from external sources as possible. In practice this requires isolation. The international standard is 330 m (cf. e.g. FAO, 1992). In Denmark an isolation belt of 500 m is recommended. Natural regeneration should be preferred if the ecological conditions allow. Small stands should be avoided to achieve adequate regeneration units.

In practise total isolation of sub-populations will not be achieved even with large isolation belts; and it is in fact not absolutely wanted, as some exchange of genetic material between populations will counteract loss of genetic variation, in particular where sub-populations are small (effective populations < 50), cf. e.g. Nunney and Campbell (1993). Static *ex situ* conservation measures may be considered in the presence of major background pollination, e.g. if the populations to be conserved are surrounded by large areas of hybridising material.

Tending
The need for tending will depend on species and site conditions. When tending is required, it should favour stability and regeneration. For some populations the conservation effort will consist of a certain management system, which may include e.g. cutting of competitive (invasive) species or for certain bushes, controlled animal grazing or fire.

Thinning is generally considered the most important tending intervention, in particular where it stimulates regeneration. In pure stands systematic thinning is usually recommended in order to maintain the genetic constitution. Systematic thinning may however tend to counteract natural selection and is thus a means favouring static conservation. Where evolutionary conservation is the purpose, thinning should in principle support naturally selective forces and may therefore not be purely systematic. In mixed stands thinning and regulation of species composition should be undertaken with much caution as it can be of more harm than use. An example from mixed dipterocarp forest in Malesia, where thinning in favour of a few priority species may reduce flowering and seed set due to the interdependency of the dipterocarps in their flowering and pollination biology (Lillesøe 1996), was mentioned in section 6.1.1.

Utilisation
In some cases, the conservation effort can be combined with different forms of forest utilisation if the use does not change the genetic constitution of the stands markedly. In some cases, conservation may be combined with ordinary forest management.

Site conditions

For *in situ* conservation and existing stands that are of potential for being considered as *ex situ* conservation stands, site conditions are naturally given. The conservation status and the expected long term development will to the extent possible be taken into consideration in the process of selecting such stands for conservation (cf. section 5). Management of *in situ* stands may require management of surrounding areas as well (see e.g. Sayer 1991).

For the establishment of *ex situ* stands, areas that will ensure good protection as well as healthy long term development should be chosen. Environmental conditions should be as similar to the original as possible. Land tenure conditions will have to be taken into consideration as well (cf. section 7.1).

8.2 Gene banks

Ex situ conservation of forest genetic resources in gene banks is an important complementary measure to the use of conservation stands. *Ex situ* storage of seeds, pollen and in vitro cultures of forest genetic resources are described in detail by Wang *et al.* (1993). Otherwise the development of gene bank technology has primarily taken place in agriculture (cf. section 6.4).

The term 'gene bank' may have a connotation of high tech. It is however not necessarily the case. Fairly simple storage facilities can be used for *ex situ* conservation of many species and are often available. More specialised structures may be required in some cases and may only be available at international level. Documentation requirements and methodology are in principle the same and the purpose of this section is not only to provide management guidelines but also to familiarise foresters working with conservation of genetic resources with the general gene bank terminology.

Gene bank technology for genetic conservation has been developed and documented since the early 1970's to a large extent under the auspices of IPGRI (formerly IBPGR) and FAO. The most recent gene bank standards were published in 1994 (FAO/IPGRI 1994).

Gene banks or genetic resource centres operate with different types of collections for different purposes, see box 5. The collections should be managed for conservation and use to fulfil the different purposes. The viability and genetic integrity of the stored material should be monitored and documented.

BOX 5. TYPES OF COLLECTIONS

Gene banks or genetic resource centres operate with different types of collections for different purposes (cf. e.g. IBPGR 1982, NRC 1993).

Base collections provide for the long term conservation of genetic material through storage under optimal conditions.

Duplicate or *back-up collections* of the base collections are kept at another location for security.

Active collections provide seeds or other propagules for distribution to plant breeders or other users. The active collections may include the same material as the base collections, but are typically for medium-term conservation, regeneration, multiplication and distribution, and evaluation.

Working collections, also called breeder's collections or research collections include materials of frequent use in breeding programmes and are usually short term in nature. Breeder's collections are often regarded as outside the framework of gene banks.

Genetic stocks consist of elite and current breeder's lines and mutants.

Field gene banks are often referred to as living collections. The term living collections as opposed to other types of gene bank collections is somewhat misleading, as the reproductive material in gene banks is also alive. The so-called living collections consist of plants, typically growing in the nursery or in the field. Field gene banks may in some cases be considered as conservation stands.

Clone banks are one type of field gene banks and may serve different purposes. They may constitute working collections of superior individuals meant for multiplication (cf. e.g. Zabala 1994), but can also be for conservation of specific genotypes (e.g. horticultural 'cultivars' (Given 1994)), or other material requiring vegetative propagation.

Managing the collections may include: collection, monitoring storage conditions, viability monitoring, regeneration and multiplication, characterisation and evaluation, and documentation and information (IBPGR 1982, NRC 1993, FAO/IPGRI 1994).

Collection involves survey or inventory of the geographical and ecological distribution of a species, usually referred to as exploration, followed by sampling between and within populations, and finally collection. Exploration and sampling are dealt with in section 5 and 6. Detailed technical guidelines and references have recently been provided in an important reference work by Guarino et al. (1995).

Storage conditions may vary according to type of collection. Standards are given by FAO/IPGRI (1994) and detailed guidelines for design of storage facilities by IBPGR (1982 and 1985c) and Stubsgaard (1992).

Viability will usually be assessed by means of germination test. Standards according to FAO/IPGRI (1994). General and specific guidelines are given e.g. by IBPGR (1985b), ISTA (1993) and Poulsen (1994).

Regeneration is needed to ensure that seeds stored do not fall below acceptable levels of viability. At the same time regeneration procedures should ensure that the genetic integrity (i.e. keep the genetic composition unchanged) of accessions is maintained (FAO/IPGRI 1994). An overview of principles involved in maintaining genetic integrity during seed regeneration can be found in NRC (1993). Regeneration is generally not a feasible management tool for trees (long-living perennials).

To maintain the genetic integrity, it is usually recommended that the regeneration should be kept to a minimum. Evolutionary conservation would, however, speak in favour of regular regeneration, but would then require collection, storage and maintenance of samples of larger effective population size (cf. section 6.1.4).

Multiplication is the same as regeneration but done with the objective of producing more reproductive material for the purpose of practical utilisation.

Characterisation is a systematic recording of selected morphological and agronomic traits of an accession. Characterisation can be carried out concurrently with regeneration (NRC 1993). Applicability of characterisation data can be ensured by standardised descriptors. IPGRI has published descriptor lists of a number of major crops.

Evaluation comprise collection and analysis of data, typically in controlled experiments and is in general a prerequisite for the wise use of conserved germplasm. Normally, evaluation in the strict sense falls outside the scope of gene banks. The initial phase of preliminary evaluation should, however, preferably take place during the first cycle of multiplication-regeneration (NRC 1993). The scientific background for regeneration and multiplication in gene banks are described by Breese (1989).

Documentation is absolutely critical in all phases of managing genetic resources. Information standards are summarised by FAO/IPGRI (1994). Relevant documentation systems are given e.g. by Kanopka and Hanson (1984), Hintum and Hazekamp (1992 and 1993), Filer (1990), Lauridsen (1994).

Hintum and Hazekamp (1993) is a good example of a national gene bank protocol covering all the above aspects. A well documented national programme of germplasm maintenance is the U.S. National Plant Germplasm System (NRC 1991b, Shands and Sisson 1989).

For woody perennials with focus on developing countries, two series of technical and lecture notes from Danida Forest Seed Centre cover the practical aspects of seed handling (DFSC).

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